

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model
Run on: January 5, 2006, 16:07:38 ; Search time 4844 Seconds
(without alignments)
2522.986 Million cell updates/sec

Title: US-09-977-579A-2
Perfect score: 1124
Sequence: 1 MPANRRLPLASLVLIVWS.....SDYLAIPSENKENSAPVPEE 215

Scoring table:
BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Xgapop 10.0 , Xgapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 5883141 seqs, 28421725653 residues
Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-DB=GenEmbl -QMT=fastcap -SUFFIX=rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOALIGN=200 -THR SCORES=500 -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
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-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : GenEmbl.*

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2: gb.in.*
3: gb.env.*
4: gb.om.*
5: gb.ov.*
6: gb.pat.*
7: gb.ph.*
8: gb.pr.*
9: gb.ro.*
10: gb.sts.*
11: gb.sy.*
12: gb.un.*
13: gb.vi.*
14: gb.htg.*
15: gb.pl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1124	100.0	1261	6	AR359850 Sequence
2	1124	100.0	1261	6	AX039100 Sequence
3	1124	100.0	1261	8	AJ243396 Homo sapi

4	1124	100.0	5306	8	AB032984	AB032984 Homo sapi
5	1116	99.3	3296	8	AB097521	AB097521 Macaca fa
6	1105	98.3	645	6	AX048004	AX048004 Sequence
7	1105	98.3	2220	6	AR359849	AR359849 Sequence
8	1105	98.3	2220	6	AX039099	AX039099 Sequence
9	1105	98.3	2220	9	RNO243395	AJ243395 Rattus no
10	1105	98.3	2632	6	AX048005	AX048005 Sequence
11	1105	98.3	3107	9	AF378093	AF378093 Rattus no
12	1105	98.3	3108	6	AX047984	AX047984 Sequence
13	1105	98.3	3910	9	BC070899	BC070899 Rattus no
14	1097	97.6	4025	9	AK173115	AK173115 Mus muscu
15	1097	97.6	4169	9	BC053919	BC053919 Mus muscu
16	1097	97.6	4176	9	BC058636	BC058636 Mus muscu
17	1091	97.1	670	9	AY049036	AY049036 Mus muscu
18	1028	91.5	606	6	CQ728741	CQ728741 Sequence
19	857	76.2	922	5	BX935227	BX935227 Gallus ga
20	755	67.2	912	5	BX931708	BX931708 Gallus ga
21	743	66.1	1736	5	BC088017	BC088017 Xenopus t
22	742	66.0	471	6	BD059018	BD059018 Secreted
23	714	63.5	1654	5	BC077295	BC077295 Xenopus l
24	477	42.4	657	4	OCU35382	U35382 Oryctolagus
25	477	42.4	657	6	AX048006	AX048006 Sequence
26	473	42.1	1335	8	HUMVSC1B	L16242 Homo sapien
27	473	42.1	1404	8	HUMSCN1BA	L10338 Human sodiu
28	473	42.1	1525	8	BC067122	BC067122 Homo sapi
29	472	42.0	701	4	DQ061859	DQ061859 Canis fam
30	472	42.0	1490	6	AX401978	AX401978 Sequence
31	472	42.0	1490	9	RATSCH1B	M91808 Rattus norv
32	472	42.0	1527	9	BC094523	BC094523 Rattus no
33	471	41.9	657	8	BT019923	BT019923 Homo sapi
34	471	41.9	657	11	AY888280	AY888280 Synthetic
35	471	41.9	1557	9	BC039140	BC039140 Mus muscu
36	470	41.8	617	6	CQ722293	CQ722293 Sequence
37	468	41.6	1125	9	MMU46681	U46681 Mus musculu
38	468	41.6	1340	9	MMU85786	U85786 Mus musculu
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42	400.5	35.6	174285	14	AC145484	AC145484 Lemur cat
43	400.5	35.6	238861	14	AC148331	AC148331 Mus muscu
44	400	35.6	214306	14	AC128723	AC128723 Rattus no
45	398.5	35.5	286712	14	AC157079	AC157079 Bos tauru

ALIGNMENTS

RESULT 1
AR359850
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
ORIGIN

AR359850
Sequence 4 from patent US 6593565.
AR359850
AR359850.1 GI:33766660
Unknown.
Unclassified.
1 (bases 1 to 1261)
Heslin,P. and Lynam,N.R.
Vehicle interior rearview mirror assembly including an
accessory-containing housing
Patent: US 6593565-A 4 15-JUL-2003;
Donnelly Corporation; Holland, MI
Location/Qualifiers
1..1261
/organism="unknown"
/mol_type="genomic DNA"

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Percent Similarity:	100.00%	Mismatches:	0
Best Local Similarity:	100.00%		

Query Match:	100.00%	Indels:	0
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US-09-977-579A-2 (1-215) x AR359850 (1-1261)			
Qy	1	MetProAlaPheAnArgLeuPheProLeuAlaSerLeuValLeuIleTyrTrpValSer	20
Db	376	ATGCTGCTTCAATAGATTGTTCCCTGCTTCTCTCGTGTATCTACTGGGTCACT	435
Qy	21	ValCysPheProValCysValGluValProSerGluThrGluAlaValGlnGlyAsnPro	40
Db	436	GTCTGCTTCCCTGTGTGTAAGTGCCTCGAGACGGAGCGCTGCGGGCAACCCC	495
Qy	41	MetLysLeuArgCysIleSerCysMetLysArgGluGluValGluAlaThrValVal	60
Db	496	ATGAAGCTGCGCTCATCTCTCGCATGAAGAGAGAGAGGTGGAGGCCACACCGTGGTG	555
Qy	61	GluTrpPheTyrArgProGluGlyClyLysAspPheLeuIleTyrGluTyrArgAsnGly	80
Db	556	GAATGGTTCACAGCCCGAGCGGTAAAGATTTCCTTATTACGAGTATCGGAATGGC	615
Qy	81	HisGlnGluValGluSerProPheGlnGlyArgLeuGlnTrpAsnGlySerLysAspLeu	100
Db	616	CACCAGGAGGTGGAGAGCCCTTTTCAGGGCGCTTCAGTGGATGGCAGGACCTG	675
Qy	101	GlnAspValSerIleThrValLeuAsnValThrLeuAsnAspSerGlyLeuTyrThrCys	120
Db	676	CAGGACGTGTCATCACTCAACGTCACTCTGAACGACTCTGCGCTCTACACCTGC	735
Qy	121	AsnValSerArgGluPheGluPheGluAlaHisArgProPheValLysThrArgLeu	140
Db	736	AATGTGTCCTGGAGTTTGTAGTTTGAGCGCATCGCCCTTTGTGAAGACACCGCGCTG	795
Qy	141	IleProLeuArgValThrGluAlaGlyGluAspPheThrSerValValSerGluIle	160
Db	796	ATCCCCCTAAGAGTCACCGAGGAGCTGGAGAGCTTCACCTCTGTGTCTCAGAAATC	855
Qy	161	MetMetTyrIleLeuLeuValPheLeuThrLeuTrpLeuLeuIleGluMetIleTyrCys	180
Db	856	ATGATGTACATCTCTGCTCTCCTCACTCTGAGAGAGCTTCACCTCTGTGTCTCAGAAATC	915
Qy	181	TyrArgLysValSerLysAlaGluAlaGlnGluAlaSerLysAspTyrLeuAla	200
Db	916	TACAGAAAGTCTCAAAAGCCGAGAGACGCCCAAGAAACGGCTCTGACTACTCTGCC	975
Qy	201	IleProSerGluAsnLysGluAsnSerAlaValProValGluGlu	215
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LOCUS			
DEFINITION	Sequence 4 from Patent WO0063367.		
ACCESSION	AX039100		
VERSION	AX039100.1	GI:11229276	
KEYWORDS			
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;		
	Hominidae; Homo.		
REFERENCE			
AUTHORS	1		
TITLE	Cox, P., Dixon, A., Jackson, A. and Morgan, K.		
	A novel family of beta sub-unit proteins from a voltage-gated sodi		
	um channel, nucleic acids encoding them and therapeutic or		
	diagnostic uses thereof		
JOURNAL	Patent: WO 0063367-A 4 26-OCT-2000;		
	WARNER-LAMBERT COMPANY (US) ; Cambridge University Technical		
	Services Limited (GB)		
FEATURES			
source	1. .1261		
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	/mol_type="unassigned DNA"		
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ORIGIN			
Alignment Scores:			
Pred. No.:	2.78e-117	Length:	1261
Score:	1124.00	Matches:	215
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	6	Gaps:	0
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Qy	21	ValCysPheProValCysValGluValProSerGluThrGluAlaValGlnGlyAsnPro	40
Db	436	GTCTGCTTCCCTGTGTGTAAGTGCCTCGAGACGGAGCGCTGCGGGCAACCCC	495
Qy	41	MetLysLeuArgCysIleSerCysMetLysArgGluGluValGluAlaThrValVal	60
Db	496	ATGAAGCTGCGCTCATCTCTCGCATGAAGAGAGAGAGGTGGAGGCCACACCGTGGTG	555
Qy	61	GluTrpPheTyrArgProGluGlyClyLysAspPheLeuIleTyrGluTyrArgAsnGly	80
Db	556	GAATGGTTCACAGCCCGAGCGGTAAAGATTTCCTTATTACGAGTATCGGAATGGC	615
Qy	81	HisGlnGluValGluSerProPheGlnGlyArgLeuGlnTrpAsnGlySerLysAspLeu	100
Db	616	CACCAGGAGGTGGAGAGCCCTTTTCAGGGCGCTTCAGTGGATGGCAGGACCTG	675
Qy	101	GlnAspValSerIleThrValLeuAsnValThrLeuAsnAspSerGlyLeuTyrThrCys	120
Db	676	CAGGACGTGTCATCACTCAACGTCACTCTGAACGACTCTGCGCTCTACACCTGC	735
Qy	121	AsnValSerArgGluPheGluPheGluAlaHisArgProPheValLysThrArgLeu	140
Db	736	AATGTGTCCTGGAGTTTGTAGTTTGAGCGCATCGCCCTTTGTGAAGACACCGCGCTG	795
Qy	141	IleProLeuArgValThrGluAlaGlyGluAspPheThrSerValValSerGluIle	160
Db	796	ATCCCCCTAAGAGTCACCGAGGAGCTGGAGAGCTTCACCTCTGTGTCTCAGAAATC	855
Qy	161	MetMetTyrIleLeuLeuValPheLeuThrLeuTrpLeuLeuIleGluMetIleTyrCys	180
Db	856	ATGATGTACATCTCTGCTCTCCTCACTCTGAGAGAGCTTCACCTCTGTGTCTCAGAAATC	915
Qy	181	TyrArgLysValSerLysAlaGluAlaGlnGluAlaSerLysAspTyrLeuAla	200
Db	916	TACAGAAAGTCTCAAAAGCCGAGAGACGCCCAAGAAACGGCTCTGACTACTCTGCC	975
Qy	201	IleProSerGluAsnLysGluAsnSerAlaValProValGluGlu	215
Db	976	ATCCCATCTGAGAACAGAGAACTCTGCGGTACCACTGGAGGAA	1020
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LOCUS			
DEFINITION	Homo sapiens mRNA for voltage-gated sodium channel beta-3 subunit		
ACCESSION	U043396		
VERSION	U043396.2	GI:7242612	
KEYWORDS	scn3b gene; voltage-gated sodium channel beta-3 subunit.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;		
	Hominidae; Homo.		
REFERENCE			
AUTHORS	1		
TITLE	Morgan, K., Stevens, E.B., Shaw, B., Cox, P., Dixon, A.K., Lee, K.,		
	Pinnock, R.D., Hughes, J., Richardson, P.J., Mizuguchi, K. and		

Jackson, A.P.
beta 3: an additional auxiliary subunit of the voltage-sensitive sodium channel that modulates channel gating with distinct kinetics
Proc. Natl. Acad. Sci. U.S.A. 97 (5), 2308-2313 (2000)
10688874

2
Direct Submission
Morgan, K.
Submitted (28-JUN-1999) Morgan K., Biochemistry, University of Cambridge, Tennis Court Road, Cambridge, CB2 1QW, UNITED KINGDOM
Revised by [4]
3 (bases 1 to 1261)
Morgan, K.
Direct Submission
Submitted (13-MAR-2000) Morgan K., Biochemistry, University of Cambridge, Tennis Court Road, Cambridge, CB2 1QW, UNITED KINGDOM
On Mar 14, 2000 this sequence version replaced gi:1160974.
Location/Qualifiers
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376..1023
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/evidence=experimental
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1025..>1261
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3' UTR
ORIGIN

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Score: 1124.00 Matches: 215
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 8 Gaps: 0

US-09-977-579A-2 (1-215) x HSA243396 (1-1261)

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Db 376 ATGCCTGCCTTCAATAGATTGTTCCCTCGGCTTCTCTGCTTATCTACTGGGTCACT 435

QY 21 ValCysPheProValCysValGluValProSerGluThrGluAlaValGlnGlyAsnPro 40
Db 436 GTCTGCTTCCCTGTGTGTGTGAAGTGCCTTGGAGACGGAGCCGTGCGAGGCAACCCC 495

QY 41 MetLysLeuArgCysIleSerCysMetLysArgGluGluValGluAlaThrThrValVal 60
Db 496 ATGAAGCTGGCTGCATCTCTCGTCATGAAGAGAGAGAGAGTGGAGGCCACCCAGGTGGT 555

QY 61 GluTrpPheTyrArgProGluGlyGlyLysAspPheLeuIleTyrGluTyrArgAsnGly 80
Db 556 GAATGGTTCTACAGGCCCGGCGGTAAGATTCTCTTATTTACGAGTATCGAATGGC 615

QY 81 HisGlnGluValGluSerProPheGlnGlyArgLeuGlnTrpAsnGlySerLysAspLeu 100

Db 616 CACCAGAGGTGGAGAGCCCTTTTCAGGGGGCCCTCAGTGGGAATGGCAGCAAGACCTG 675
QY 101 GluAspValSerIleThrValLeuAsnValThrLeuAsnAspSerGlyLeuTyrThrCys 120
Db 676 CAGGACGTGTCATCACTGCTCAAGTCACTCTGAACGACTCTGGCTCTACACCTGC 735
QY 121 AsnValSerArgGluPheGluPheGluAlaHisArgProPheValLysThrArgLeu 140
Db 736 AATGTGTCCCGGAGTTTGTAGTTTGGAGCGCATCGGCCCTTTGTGAAGACACGCGGCTG 795
QY 141 IleProLeuArgValThrGluGluAlaGlyCysLysPheThrSerValValSerGluIle 160
Db 796 ATCCCCCTAAGAGTCACCGAGGAGCGCTGGAGAGACTTCACCTCTGTGTGCTCAGAAATC 855
QY 161 MetMetTyrIleLeuValPheLeuThrLeuTyrTrpLeuLeuIleGluMetIleTyrCys 180
Db 856 ATGATGTACATCTCTTCTGCTTCTCACCCTGTGGCTGCTCATCGAGATGATATATTGC 915
QY 181 TyrArgLysValSerLysAlaGluGluAlaGlnGluAsnAlaSerAspTyrLeuAla 200
Db 916 TACAGAAAGGTCTCAAAAGCCGAAAGAGGAGCGCCCAAGAAACGGCTCTGACTTACCTTGC 975
QY 201 IleProSerGluAsnLysGluAsnSerAlaValProValGluGlu 215
Db 976 ATCCCATCTGAGAACAAAGGAGACTCTGCGGTACCGAGTGGAGGAA 1020

RESULT 4
AB032984 5306 bp mRNA linear PRI 11-NOV-1999
LOCUS Homo sapiens mRNA for KIAA1158 protein, partial cds.
DEFINITION AB032984
ACCESSION AB032984.1 GI:6330135
VERSION
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (sites)
Hirosewa, M., Nagase, T., Ishikawa, K., Kikuno, R., Nomura, N. and
Ohara, O.
Characterization of cDNA clones selected by the GeneMark analysis
from size-fractionated cDNA libraries from human brain
DNA Res. 6 (5), 329-336 (1999)
10574461
2 (bases 1 to 5306)
Ohara, O., Nagase, T. and Kikuno, R.
Direct Submission
Submitted (04-OCT-1999) Osamu Ohara, Kazusa DNA Research Institute,
Laboratory of DNA Technology, 1532-3 Yana, Kisarazu, Chiba
292-0812, Japan (E-mail:cdnaifoo@kazusa.or.jp,
URL: http://www.kazusa.or.jp/huge/, Tel: +81-438-52-3913,
Fax: +81-438-52-3914)
Location/Qualifiers
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/dev_stage="adult"
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ENKENSAPVVEE"

ORIGIN		Alignment Scores:		1.59e-116		Length: 5306	
Pred. No.:		Score:		1124.00		Matches: 215	
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DB:							
US-09-977-579A-2 (1-215) x AB032984 (1-5306)							
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Db	48	ATGCCTGCCTTCAATAGATTGTTTCCCTGGCTTCTCTCGTGCTTATCTACTGGGTCACT	107				
Qy	21	ValCysPheProValCysValGluValProSerGluThrGluAlaValGlnGlyAsnPro	40				
Db	108	GTCTGCTTCCCTGTGTGTGGAAGTGCCCTCGAGACGGAGCGCGTGCGAGGGCAACCCC	167				
Qy	41	MetLysLeuArgCysIleSerCysMetLysArgGluGluValGluAlaThrThrValVal	60				
Db	168	ATGAAGCTGGCTGCATCTCTCGATGAAGAGAGAGAGGTGGAGGCCACACCGTGGTG	227				
Qy	61	GluTrpPheTyrArgProGluGlyGlyLysAspPheLeuIleTyrGluTyrArgAsnGly	80				
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Qy	81	HisGlnGluValGluSerProPheGlnGlyArgLeuGlnTrpAsnGlySerLysAspLeu	100				
Db	288	CACCAGGAGTGGAGAGCCCTTTTCAGGGCGGCTGCAGTGAATGGCAGCAAGGACCTG	347				
Qy	101	GlnAspValSerIleThrValLeuAsnValThrLeuAsnAspSerGlyLeuTyrThrCys	120				
Db	348	CAGGAGCTGTCCATCACTGTGCTCAACGTCACCTCTGAACGACTCTGGCCTCTACACCTGC	407				
Qy	121	AsnValSerArgGluPheGluAlaHisArgProPheValLysThrThrArgLeu	140				
Db	408	AATGTGTCCTCCGGAGTTTGTAGTTTGAGCGCATCGGCCCTTTGTGAAGACGACGCGCTG	467				
Qy	141	IleProLeuArgValThrGluGluAlaGlyGluAspPheThrSerValValSerGluIle	160				
Db	468	ATCCCTTAAGAGTCAAGAGGAGGCTGGAGAGGACTTCACCTCTGTGGTCTCAGAAATC	527				
Qy	161	MetMetTyrIleLeuLeuValPheLeuThrLeuTrpLeuLeuIleGluMetIleTyrCys	180				
Db	528	ATGATGTACATCTCTGGTCTTCCTCACCTTGTGGCTGCTCATCGAGATGATATATGTC	587				
Qy	181	TyrArgLysValSerLysAlaGluGluAlaAlaGlnGluAsnAlaSerAspTyrLeuAla	200				
Db	588	TACAGAAAGTCTCAAAAGCCGAAGAGGACCCCAAGAAACGGCTCTGACTACTTGGCC	647				
Qy	201	IleProSerGluAsnLysGluAsnSerAlaValProValGluGlu	215				
Db	648	ATCCCATCTGAGAACAGAGAACTCTGCGGTACCACTGGAGGAA	692				

RESULT 5
AB097521
LOCUS
DEFINITION
Macaca fascicularis brain cDNA clone:QmoA-13657, similar to human voltage-gated sodium channel beta-3 subunit (SCN3B), mRNA, NM_018400.
AB097521
ACCESSION
VERSION
AB097521.1 GI:26449236
KEYWORDS
oligo capping; fis (full insert sequence).
SOURCE
Macaca fascicularis (crab-eating macaque)
ORGANISM
Macaca fascicularis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Cercopithecoidea; Cercopithecinae; Macaca.
1
Ooada,N., Hida,M., Kusuda,J., Tanuma,R., Iseki,K., Hirata,M., Suto,Y., Hirai,M., Terao,K., Suzuki,Y., Sugano,S. and Hashimoto,K. Assignment of 118 novel cDNAs of cynomolgus monkey brain to human chromosomes
Gene 275 (1), 31-37 (2001)
11574149
2 (bases 1 to 3296)
Hashimoto,K., Ooada,N., Hida,M., Kusuda,J. and Sugano,S. Direct Submission
Submitted (05-DEC-2002) Katsuyuki Hashimoto, National Institute of Infectious Diseases, Division of Genetic Resources; 23-1, Toyama 1-chome, Shinjuku-ku, Tokyo, 162-8640, Japan
(E-mail:khashi@nih.go.jp, URL:http://www.nih.go.jp/yoken/genebank/, Tel:81-3-5285-1111(ex.2120), Fax:81-3-5285-1181)
Lab host: TOP10
Vector: pME18S-FL3 (Acc.No. AB009864)
R. Site: DraIII (CACGTGTG)
R. Site: DraIII (CACGATGG)
Description: 1st strand cDNA was primed with an oligo(dT) primer [ATGCGCTTTTCTTTTCTTTT]; double-stranded cDNA was synthesized using specific 5' and 3' primers and amplified by PCR. The PCR product was digested with SfiI and size selection was performed to exclude fragments <1.5kb.The SfiI-digested PCR product was cloned into distinct draIII sites of pME18S-FL3. XhoI sites just outside the draIII sites can be used to isolate the cDNA insert. Libraries were constructed by oligo-capping method. Custom primers used for sequencing (5' end primer [CTTCTGCTCTAAAGCTGCG]; 3' end primer [CGACCTGCAGCTCGAGCACA]).
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/note="similar to human voltage-gated sodium channel beta-3 subunit (SCN3B), mRNA, NM_018400"
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Alignment Scores:
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Query Match: 99.29% Indels: 0
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DEFINITION Sequence 3 from Patent WO0063367.
ACCESSION AX039099
VERSION AX039099.1 GI:11229275
KEYWORDS
SOURCE Rattus sp.
ORGANISM Rattus sp.
REFERENCE
AUTHORS Cox, P., Dixon, A., Jackson, A. and Morgan, K.
TITLE A novel family of beta sub-unit proteins from a voltage-gated sodi
um channel, nucleic acids encoding them and therapeutic or
diagnostic uses there of
JOURNAL Patent: WO 0063367-A 3 26-OCT-2000;
WARNER-LAMBERT COMPANY (US) ; Cambridge University Technical
Services Limited (GB)
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DEFINITION Rattus norvegicus mRNA for voltage-gated sodium channel beta-3 subunit.
ACCESSION AJ243395
VERSION AJ243395.2 GI:7242802
KEYWORDS scn3b gene; voltage-gated sodium channel beta-3 subunit.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Rattus.
1
REFERENCE
AUTHORS Morgan, K., Stevens, E.B., Shaw, B., Cox, P., Dixon, A.K., Lee, K.,
Pinnock, R.D., Hughes, J., Richardson, P.J., Mizuguchi, K. and
Jackson, A.P.
TITLE beta 3: an additional auxiliary subunit of the voltage-sensitive
sodium channel that modulates channel gating with distinct kinetics
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (5), 2308-2313 (2000)
PUBMED 10688874
REFERENCE 2

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AUTHORS Morgan, K.
TITLE Direct Submission
JOURNAL Submitted (28-JUN-1999) Morgan K., Biochemistry, University of Cambridge, Tennis Court Road, Cambridge, CB2 1QW, UNITED KINGDOM
REMARK Revised by [3]
REFERENCE 3 (bases 1 to 2220)
AUTHORS Morgan, K.
TITLE Direct Submission
JOURNAL Submitted (09-MAR-2000) Morgan K., Biochemistry, University of Cambridge, Tennis Court Road, Cambridge, CB2 1QW, UNITED KINGDOM
COMMENT On Mar 14, 2000 this sequence version replaced gi:7161888.
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Best Local Similarity: 98.14% Mismatches: 4
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DB 363 ATGCCTGCCTTCAACAGATTGCTCCCTAGCTTCTTAGTGTCTCATCTACTGGGTGAGA 422
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QY 41 MetLysLeuArgCysIleSerCysMetLysArgGluGluValGluAlaThrThrValVal 60
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RESULT 10
AX048005
LOCUS Sequence 22 from Patent WO0069912.
DEFINITION AX048005
ACCESSION AX048005.1 GI:11876883
VERSION
KEYWORDS
SOURCE Rattus sp.
ORGANISM Rattus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Rattus.
REFERENCE
1
AUTHORS Curtis, R.A.
TITLE Gene encoding a sodium channel beta-3 subunit protein
JOURNAL Patent: WO 0069912-A 22 23-NOV-2000;
Millennium Pharmaceuticals, Inc. (US)
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LOCUS
DEFINITION Rattus norvegicus sodium channel beta 3 subunit (SCN3B) mRNA,
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ACCESSION AF378093
VERSION AF378093.1 GI:14165175
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SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Rattus.
Q.Y., Curtis, R., Lawson, D., Gilbride, K., Ge, P., DiStefano P, S.,
Silos-Santiago, I., Catterall W, A. and Scheuer, T.
Differential modulation of sodium channel gating and persistent
sodium currents by the beta1, beta2, and beta3 subunits
Mol. Cell. Neurosci. 18 (5), 570-580 (2001)
11922146
PUBMED
REFERENCE 2 (bases 1 to 3107)
Curtis, R.
Direct Submission
TITLE Submitted (05-MAY-2001) Neurobiology, Millennium Pharmaceuticals
Inc., 75 Sidney Street, Cambridge, MA 02139, USA
JOURNAL Location/Qualifiers
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ACCESSION AX047984
VERSION AX047984.1 GI:11876881
KEYWORDS
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Rattus.
1
Curtis, R. A.
Gene encoding a sodium channel beta-3 subunit protein
Patent: WO 0069912-A 1 23-NOV-2000;
Millennium Pharmaceuticals, Inc. (US)
Location/Qualifiers
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ORIGIN

Alignment Scores:
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Best Local Similarity: 98.14% Mismatches: 4
Query Match: 98.31% Indels: 0
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US-09-977-579A-2 (1-215) x AX047984 (1-3108)

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Db 618 TACAGAAAGTCTCTTAAGCCCGAGAGGAGGACACAGGAAATGCGTGTGACTACCTTGTCT 677
Qy 201 IleProSerGluAsnLysGluAsnSerAlaValProValGluGlu 215
Db 678 ATCCCTTTCAGAGAACAGAGAACTCTGTGGTACCTGTGGAGGAA 722

RESULT 13
BC070899
LOCUS
DEFINITION
Rattus norvegicus sodium channel, voltage-gated, type III, beta,
mRNA (cDNA clone MGC:91409 IMAGE:7100476), complete cds.
ACCESSION
BC070899
VERSION
BC070899.1 GI:47477789
KEYWORDS
MGC.
SOURCE
Rattus norvegicus (Norway rat)
ORGANISM
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Rattus.

REFERENCE
AUTHORS

1 (bases 1 to 3910)
Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Haieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Ustin, T.B., Loquellano, N.A., Peters, G.J.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Kettman, M., Madan, A., Young, A.C., Shvachenko, Y.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shvachenko, Y.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smalusz, D.E.,
Schnurch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
12477932
2 (bases 1 to 3910)
Director MGC Project.
Direct Submission
Submitted (17-MAY-2004) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgapbs-re@mail.nih.gov
Tissue Procurement: Howard Jacobs
cDNA Library Preparation: Express Genomics
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: <http://www.nisc.nih.gov/>
Contact: nisc_mgc@nigr.nih.gov
Akhter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B.,
Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S.,
Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P.,
Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R.,
Maduro, Q.L., Masiello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C.,
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Young, A., Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAP Place: 175 Row: 9 Column: 5
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 47575878.

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CDS

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ORIGIN

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Percent Similarity:	98.14%	Mismatches:	4
Best Local Similarity:	98.14%	Indels:	0
Query Match:	98.31%	Gaps:	0
DB:	9		

US-09-977-579A-2 (1-215) x BC070899 (1-3910)

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Qy	21	ValCysPheProValCysValGluValProSerGluThrGluAlaValGlnGlyAsnPro	40
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Qy	41	MetLysLeuArgCysIleSerCysMetLysArgGluValGluAlaThrThrValVal	60
Db	498	ATGAAGCTGAGGTGCATCTCTGTCATGAAGAGGAGGAGGTGGAGGCCACCACTGTGGTG	557
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Qy	121	AsnValSerArgGluPheGluPheGluAlaHisArgProPheValysThrThrArgLeu	140
Db	738	AATGTGTCTCAGGAGATTCTGAATTCGAGGCCACACAGGCCCTTTGTGGAAGACCAGAGACTG	797
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RESULT 14
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 LOCUS
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 DEFINITION
 AKI73115
 ACCESSION
 VERSION
 GI:50510814
 FLI CDNA.
 KEYWORDS
 Mus_musculus (house mouse)
 SOURCE

AKI73115
 Mus musculus mRNA for mK1AA1158 protein.
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 GI:50510814
 FLI CDNA.
 KEYWORDS
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 SOURCE

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AKI73115
 Mus musculus mRNA for mK1AA1158 protein.
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 Mus_musculus (house mouse)
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AKI73115
 Mus musculus mRNA for mK1AA1158 protein.
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ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
AUTHORS
Okazaki, N., F-Kikuno, R., Ohara, R., Inamoto, S., Koseki, H.,
Hiraoka, S., Saga, Y., Seino, S., Nishimura, M., Kaisho, T., Hoshino, K.,
Kitamura, H., Nagase, T., Ohara, O. and Koga, H.
Prediction of the coding sequences of mouse homologues of KIAA
gene: IV. The complete nucleotide sequences of 500 mouse
KIAA-homologous cDNAs identified by screening of terminal sequences
of cDNA clones randomly sampled from size-fractionated libraries
DNA Res. 11 (3), 205-218 (2004)

JOURNAL
PUBMED
15368895
2 (bases 1 to 4025)
REFERENCE
AUTHORS
Okazaki, N., Kikuno, R. F., Nagase, T., Ohara, O. and Koga, H.
Direct Submission
Submitted (19-MAY-2004) Hisashi Koga, Kazusa DNA Research
Institute, Laboratory for Genome Informatics, 2-6-7
Kazusa-kamatori, Kisarazu, Chiba, 292-0818, Japan
(E-mail: mousekazusa.or.jp, Tel: 81-438-52-3919, Fax: 81-438-52-3918)
The CREATE program supported by Japan science and technology
corporation; cDNA full insert sequencing; Kazusa DNA Research
Institute; cDNA library construction, clone selection and 5'- &
3'-end one pass sequencing.

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Alignment Scores:
Pred. No.: 1,3e-113 Length: 4025
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DB: Gaps: 0
US-09-977-579A-2 (1-215) x AKI73115 (1-4025)

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BC053919 4169 bp mRNA linear ROD 08-OCT-2003
BC053919 Mus musculus sodium channel, voltage-gated, type III, beta, mRNA
DEFINITION (cDNA clone MGC:56857 IMAGE:6308278), complete cds.
ACCESSION BC053919.1 GI:32172797
VERSION BC053919.1
KEYWORDS MGC.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Murioidea; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 4169)
AUTHORS Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, P.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
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Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
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Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
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Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Small, D.E.,
Schnurch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
12477932
2 (bases 1 to 4169)
REFERENCE Strausberg, R.
AUTHORS Direct Submission
TITLE Submitted (16-JUN-2003) National Institutes of Health, Mammalian
Genome Collection (MGC), Cancer Genomics Office, National Cancer

Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-c@mail.nih.gov
Tissue Procurement: Susan L. Sullivan, PhD.
cDNA Library Preparation: Reegen, Invitrogen Corp
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Institute for Systems Biology
http://www.systemsbio.org
contact: amadan@systemsbio.org
Anup Madan, Jessica Fahney, Erin Helton, Mark Kettelman, Anuradha
Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting
Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAK Plate: 105 Row: d Column: 7
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 23943798.
Location/Qualifiers
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Score: 1097.00 Matches: 210
Percent Similarity: 97.67% Conservative: 0
Best Local Similarity: 97.67% Mismatches: 5
Query Match: 97.60% Indels: 0
DB: 9 Gaps: 0
US-09-977-579A-2 (1-215) x BC053919 (1-4169)
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 Db 608 CAGGACGTATCCATCCTGTTCTCAATGTCACCTCTGAATGACTCTGGCCTCTACACATGT 667
 Qy 121 AsnValSerArgGluPheGluPheGluAlaHisArgProPheValLysThrThrArgLeu 140
 Db 668 AATGTGTCAGGGAGTTTGTAGTTCGAAGCACACCGGCCCTTTGTGAAGACCACCAAGACTA 727
 Qy 141 IleProLeuArgValThrGluGluAlaGlyGluAspPheThrSerValValSerGluIle 160
 Db 728 ATACCCCTGCCAGTCACTGAAGAGCGGGAGAGACTTCACCTCCGTGGTCTCGGAATC 787
 Qy 161 MetMetTyrIleLeuLeuValPheLeuThrLeuTrpLeuLeuIleGluMetIleTyrCys 180
 Db 788 ATGATGTACATCCTCTGGTCTTCTCCTCACCTTGTGGCTGTTTATTGAGATGATCTATTGC 847
 Qy 181 TyrArgLysValSerLysAlaGluGluAlaGlnGluAsnAlaSerAspTyrLeuAla 200
 Db 848 TACAGAAAGGTCTCTAAGGCCGAAGAGGCACTCAGGAAATGGCTCTGACTACCTTGCT 907
 Qy 201 IleProSerGluAsnLysGluAsnSerAlaValProValGluGlu 215
 Db 908 ATCCCTTCAGAGAACAAAGGAGACTCTGTGTACCCCGTGGAGGAA 952

Search completed: January 5, 2006, 17:49:40
 Job time : 4880 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: January 5, 2006, 18:20:53 ; Search time 587 Seconds

(without alignments)
2441.071 Million cell updates/sec

Title: US-09-977-579A-2

Perfect score: 1124

Sequence: 1 MPANRLPLASLVLIIYWS.....SDYLAIPSENKENSAPVPEE 215

Scoring table:

BLOSUM62

Xgapop 10.0 , Xgapext 0.5

Ygapop 10.0 , Ygapext 0.5

Fgapop 6.0 , Fgapext 7.0

Delpop 6.0 , Delpext 7.0

Searched: 4996997 seqs, 332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-O=/cgn2.1/USPTO.spool/US09977579/runat.05012006.160651.29012/app.query.fasta.1.391
-DB=N Geneseq -QFMT=fastap -SUFFIX=rng -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNIT5=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
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-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

N_Geneseq.21.*
1: geneseqm1980s.*
2: geneseqm1990s.*
3: geneseqm2000s.*
4: geneseqm2001as.*
5: geneseqm2001bs.*
6: geneseqm2002as.*
7: geneseqm2002bs.*
8: geneseqm2003as.*
9: geneseqm2003bs.*
10: geneseqm2003cs.*
11: geneseqm2003ds.*
12: geneseqm2004as.*
13: geneseqm2004bs.*
14: geneseqm2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1124	100.0	1261	3 AAC67837	Aac67837 Human bet
2	1124	100.0	1261	10 ADB78651	Adb78651 Human ion
3	1124	100.0	1261	10 ACF57870	Acf57870 Human SCN
4	1124	100.0	1510	4 AAF84146	Aaf84146 Human nov

5	1124	100.0	4052	6 ABA93727	Aba93727 Human eig
6	1105	98.3	645	5 AAC90601	Aac90601 Rat sodiu
7	1105	98.3	2220	3 AAC67836	Aac67836 Rat beta3
8	1105	98.3	2632	5 AAC90602	Aac90602 Rat sodiu
9	1105	98.3	3108	5 AAC90600	Aac90600 Rat sodiu
10	1024	91.1	1045	4 AAK52345	Aak52345 Human pol
11	1003	89.2	978	4 AAH98320	Aah98320 Human EST
12	1003	89.2	978	13 ADS11487	Ads11487 Human the
13	975.5	82.5	1195	5 AAS86764	Aas86764 DNA encod
14	886.5	78.9	953	13 ADS10151	Ads10151 Human the
15	742	66.0	471	2 AAV86895	Aav86895 EST clone
16	694	61.7	3531	5 AAC86763	Aac86763 DNA encod
17	477	42.4	657	5 AAC90603	Aac90603 Rabbit so
18	473	42.1	1335	10 ACF57868	Acf57868 Human SCN
19	473	42.1	1335	12 ADQ19428	Adq19428 Human sof
20	473	42.1	1414	8 ABZ23837	Abz23837 Human vol
21	473	42.1	1414	14 ADY27074	Ady27074 Human SCN
22	472	42.0	1414	10 ADB78640	Adb78640 Human ion
23	472	42.0	1490	6 ABK63747	Abk63747 Rat sequ
24	472	42.0	1490	10 ADB52855	Adb52855 Primary r
25	472	42.0	1490	12 ADO09498	Ado09498 Rat sodiu
26	472	42.0	1490	13 ADV41127	Adv41127 Rat card
27	471	41.9	657	14 ADV42849	Adv42849 Human psy
28	465	41.4	1414	10 ADB78641	Adb78641 Human ion
29	408.5	36.3	621	5 AAS86762	Aas86762 DNA encod
30	262.5	23.4	850	4 AAF57675	Aaf57675 Rat sodiu
31	262.5	23.4	850	4 AAF30669	Aaf30669 Sodium ch
32	260.5	23.2	974	6 AAD29622	Aad29622 Human bet
33	234	20.8	407	4 ABA08942	Abas08942 Human vol
34	234	20.8	407	4 AAK53329	Aak53329 Human pol
35	230	20.5	855	10 ADG15041	Adg15041 Human SEC
36	218.5	19.4	358	10 ACD98234	Acd98234 Human col
37	172	15.3	747	14 AEA46527	Aea46527 Mouse mye
38	167	14.9	1029	9 ACF25382	Acf25382 Rat schwa
39	165.5	14.7	3583	12 ADQ23651	Adq23651 Human sof
40	163.5	14.5	777	6 ABA02395	Abas02395 Human mye
41	163.5	14.5	1693	12 ADF45442	Adf45442 Human vas
42	161.5	14.4	162	12 ADM66944	Adm66944 Human adi
43	160.5	14.3	970	4 AAF27741	Aaf27741 Human tra
44	160.5	14.3	983	4 AAD02925	Aad02925 Human PRO
45	160.5	14.3	983	6 ABK33654	Abk33654 cDNA enco

ALIGNMENTS

RESULT 1
AAC67837
ID AAC67837 standard; cDNA; 1261 BP.

AC AAC67837;

DT 15-FEB-2001 (first entry)

DE Human beta3 cDNA.

KW Human; beta sub-unit; beta3; analgesic; anticonvulsant;

KW cerebroprotective; vasotropic; cardiant; nootropic; cytostatic;

KW dermatological; gene therapy; voltage-gated sodium channel; pain;

KW epilepsy; stroke; ischaemia; heart disease; Jacobson Syndrome;

KW familial nonchromaffin paraganglioma; phenylketonuria;

KW Charcot Marie Tooth disease; ss.

OS Homo sapiens.

XX WO200063367-A1.

XX 26-OCT-2000.

XX 24-FEB-2000; 2000WO-EP001783.

XX 15-APR-1999; 99US-0129473P.

PA (WARN) WARNER LAMBERT CO.

PA (UYCA-) UNIV CAMBRIDGE TECH SERVICES LTD.
XX Cox P, Dixon A, Jackson A, Morgan K;
XX WPI; 2000-665241/64.
DR P-PSDB; AAB36002.
XX Novel nucleic acids encoding a beta-3 subunit from a voltage-gated sodium
PT channel, and their corresponding polypeptides, useful for detecting and
PT treating sodium channel-associated conditions, e.g. pain, epilepsy and
PT stroke.
XX
XX Claim 10; Page 70-71; 88pp; English.
XX
XX The present sequence is given in the claims of a specification relating
CC to a novel family of beta sub-unit proteins from a voltage-gated sodium
CC channel. Human and rat beta sub-units, which have been collectively
CC identified as beta3, have been isolated. The polynucleotides and
CC polypeptides are useful for screening for agonists and antagonists of
CC sodium channels. The agonists, antagonists, proteins and nucleic acids
CC may be used diagnosing of treating diseases or conditions associated with
CC voltage-gated sodium channels, e.g. pain, epilepsy, stroke, ischaemia,
CC heart disease, Jacobsen Syndrome, Familial Nonchromaffin Paraganglioma,
CC Phenylketonuria and Charcot Marie Tooth disease
XX
SQ Sequence 1261 BP; 263 A; 366 C; 372 G; 260 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 2.66e-124 Length: 1261
Score: 1124.00 Matches: 215
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-09-977-579A-2 (1-215) x AAC67837 (1-1261)

Qy 1 MetProAlaPheAsnArgLeuPheProLeuAlaSerLeuValLeuIleTyrTrpValSer 20
Db 376 ATGGCTGCTTCAATAGATTGTTTCCCTGGCTTCTCTCGTGTATCTACTGGGTGAGT 435
Qy 21 ValCysPheProValCysValGluValProSerGluThrGluAlaValGlnGlyAsnPro 40
Db 436 GTCTGCTTCCCTGTGTGTGGAGTGCCTTCGAGACGGAGCGCGTGCAGGGCAACCCC 495
Qy 41 MetLysLeuArgCysIleSerCysMetLysArgGluGluValGluAlaThrThrValVal 60
Db 496 ATGAAGCTGCCCTGCATCTCTCGCATGAAGAGAGAGAGGGTGGAGGCCACCACCGTGGTG 555
Qy 61 GluTrpPheTyrArgProGluGlyCysLysAspPheLeuIleTyrGluTyrArgAsnGly 80
Db 556 GAATGGTGTCTACAGGCCCGAGGGCGGTAAGATTTCCTTATTTACGAGTATCGGAATGCG 615
Qy 81 HisGlnGluValGluSerProPheGlnGlyArgLeuGlnTrpAsnGlySerLysAspLeu 100
Db 616 CACCAGAGGTGGAGAGGCCCTTTTCAGGGCGCCTGCAGTGGAAATGGCAGCAGACTG 675
Qy 101 GlnAspValSerIleThrValLeuAsnValThrLeuAsnAspSerGlyLeuTyrThrCys 120
Db 676 CAGGACGTGTCCATCCTGCTCAACGTCACTCTGAACGACTCTGGCTCTACACCTGCG 735
Qy 121 AsnValSerArgGluPheGluPheGluAlaHisArgProPheValLysThrThrArgLeu 140
Db 736 AATGTGTCCCGGAGTTTGTAGTTTGGAGCGCATCGGCCCTTTGTGAAGACGACCGCGCTG 795
Qy 141 IleProLeuArgValThrGluAlaGlyGluAspPheThrSerValValSerGluIle 160
Db 796 ATCCCCCTAAGAGTCAACGAGAGGCTGGAGAGACTTCACCTCTGTGGTCTCAGAAATC 855
Qy 161 MetMetTyrIleLeuLeuValPheLeuThrLeuTrpLeuLeuIleGluMetIleTyrCys 180
Db 856 ATGATGTACATCTTCTGCTTCTCCACCTGCTGGCTGCTCATCGAGATGATATATTCG 915

Qy 181 TyrArgLysValSerLysAlaGluAlaGlnGluAsnAlaSerAspTyrLeuAla 200
Db 916 TACAGAAAGGTCTCAAAAGCCGAGAGCGCCCAAGAAACGCGTCTGACTACCTTGCC 975
Qy 201 IleProSerGluAsnLysGluAsnSerAlaValProValGluGlu 215
Db 976 ATCCCATCTGAGACACAGGAGACTCTGCGGTACCACTGGAGGAA 1020
RESULT 2
ADB78651
ID ADB78651 standard; cDNA; 1261 BP.
XX
AC ADB78651;
XX
XX 04-DEC-2003 (first entry)
XX Human ion channel subunit cDNA mutant SCN1AR exon 1 SEQ ID NO:22.
DE
XX
XX ss; gene; mutant; ion channel; ion channel subunit; ICS; nootropic;
KW neuroprotective; inotropic; antipyrretic; antiarrhythmic; antimigraine;
KW antidepressant; antiparkinsonian; neuroleptic; tranquiliser; analgesic;
KW nephrotropic; antidiabetic; ophthalmological; epilepsy;
KW ion channel dysfunction; human.
XX
OS Synthetic.
OS Homo sapiens.
XX
XX WO2003008574-A1.
XX 30-JAN-2003.
PD
XX
XX 08-JUL-2002; 2002WO-AU000910.
PF
XX
XX 18-JUL-2001; 2001AU-00006452.
PR
XX
XX 05-MAR-2002; 2002AU-00000910.
PR
XX
XX 13-MAY-2002; 2002AU-00002292.
PR
XX
XX (BION-) BIONOMICS LTD.
PA
XX
XX (WALL// WALLACE R W.
XX
XX
PI Mulley JC, Harkin LA, Dibbens LM, Phillips HA, Heron SE;
XX Berkovic SF, Scheffer IE;
XX
XX WPI; 2003-239332/23.
DR
XX
XX Identifying predisposition to an ion channel dysfunction, such as
PT periodic paralysis, cardiac arrhythmias, migraine, Alzheimer's disease,
PT schizophrenia, anxiety and depression, by detecting encoding-gene
PT mutation events.
XX
XX Claim 6; SEQ ID NO 22; 106pp; English.
PS
XX
XX The invention relates to a novel method for identifying a subject
CC predisposed to a disorder associated with ion channel dysfunction. The
CC method comprises ascertaining if at least one of the genes encoding ion
CC channel subunits (ICS) has undergone a mutation event so that a cDNA
CC derived from the subject has any of 134 nucleotide sequences. The method
CC of the invention has nootropic, neuroprotective, inotropic, antipyrretic,
CC antiarrhythmic, antimigraine, antidepressant, antiparkinsonian,
CC neuroleptic, tranquiliser, analgesic, nephrotropic, antidiabetic, and
CC ophthalmological activity. A polynucleotide of the invention acts as an
CC ion channel agonist, or ion channel antagonist. The methods, isolated
CC nucleic acids, polypeptides, antibody, selective agonist, antagonist or
CC modulator of an ion channel, cells and genetically modified non-human
CC animal, are useful for the diagnosis and treatment of epilepsy and/or a
CC disorder associated with ion channel dysfunction, such as hyper- or hypo-
CC kalemic periodic paralysis, myotonias, malignant hyperthermia,
CC myasthenia, cardiac arrhythmias, episodic ataxia, migraine, Alzheimer's
CC disease, Parkinson's disease, schizophrenia, hyperkplexia, anxiety,
CC depression, phobic obsessive symptoms, neuropathic pain, inflammatory
CC pain, chronic/acute pain, Bartter's syndrome, polycystic kidney disease,
CC Dent's disease, hyperinsulinaemic hypoglycaemia of infancy, cystic
CC fibrosis, congenital stationary night blindness and total colour

CC blindness. The present sequence represents a mutant cDNA of the
CC invention. The sequence data for this patent is not represented in the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pat_sequences.

XX SQ Sequence 1261 BP; 263 A; 365 C; 372 G; 261 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 2,66e-124 Length: 1261
Score: 1124.00 Matches: 215
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps:

US-09-977-579A-2 (1-215) x ADB78651 (1-1261)

QY 1 MetProAlaPheAsnArgLeuPheProLeuAlaSerLeuValLeuIleTyrTrpValSer 20
DB 376 ATGCTGCTTCAATAGATTGTTCCCTGGCTTCTCGTGTATCTACTGGTCACT 435
QY 21 ValCysPheProValCysValGluValProSerGluThrGluAlaValGlnGlyAsnPro 40
DB 436 GTCTGCTTCCCTGTGTGTGAAGTGCCTCGAGACGGAGCGGTGCAGGCGCAACCCC 495
QY 41 MetLysLeuArgCysIleSerCysMetLysArgGluValGluAlaThrThrValVal 60
DB 496 ATGAAGCTGCGCTGCATCTCTCGCATGAAGAGAGAGAGGTGGAGCCACACGGTGGT 555
QY 61 GluTrpPheTyrArgProGluGlyGlyAspPheLeuIleTyrGluTyrArgAsnGly 80
DB 556 GAATGGTCTACAGCCCGGCGGTAAAGATTTCCTTATTACAGATATCGAATGCG 615
QY 81 HisGlnGluValGluSerProPheGlnGlyArgLeuGlnTrpAsnGlySerLysAspLeu 100
DB 616 CACCAAGAGGTGAGAGGCCCTTTCAGGGCGCTGAGTGAATGGCAGCAAGACCTG 675
QY 101 GlnAspValSerIleThrValLeuValThrLeuAsnAspSerGlyLeuTyrThrCys 120
DB 676 CAGGACGTGTCCATCACTGTCTCAACGTCATCTGAACGACTCTGGCCCTTACACCTGC 735
QY 121 AsnValSerArgGluPheGluPheGluAlaHisArgProPheValLysThrThrArgLeu 140
DB 736 ATGTGTCCGGAGTTTGTGAGTTCATGCGCATCGGCCCTTGTGAAGACGACGGCTG 795
QY 141 IleProLeuArgValThrGluGluAlaGlyGluAspPheThrSerValValSerGluIle 160
DB 796 ATCCCCCTTAAGAGTCACTCAGGAGGCTGGAGAGGACTTCACCTCTGTGTCTCAGAAATC 855
QY 161 MetMetTyrIleLeuLeuValPheLeuThrLeuThrLeuIleGluMetIleTyrCys 180
DB 856 ATGATGTACATCTCTGCTTCTCTCACCCCTGTGGCTCTCATCGAGATGATATATTC 915
QY 181 TyrArgLysValSerLysAlaGluGluAlaAlaGlnGluAlaSerAspTyrLeuAla 200
DB 916 TACAGAAAGTCTCAAAAGCCGAGAGGAGGCCCAAGAAACCGCTCTACCTTGGCC 975
QY 201 IleProSerGluAsnLysGluAsnSerAlaValProValGluGlu 215
DB 976 ATCCCATCTGAGAACAGAGAGAACTCTGCGGTACCACTGAGGAGAA 1020

RESULT 3

ACF57870

ID ACF57870 standard; cDNA; 1261 BP.

XX AC

AC ACF57870;

XX XX

DT 15-JAN-2004 (first entry)

XX XX

DE Human SCN3B protein encoding cDNA.

XX KW

SCN3B; sodium channel type 1 alpha-subunit; anticonvulsant; analgesic;
neuroprotective; anesthetic; cytosolic; cerebroprotective; cardiac;

KW hypotensive; gene therapy; SCN3B; human; gene; ss.

XX OS

XX Homo sapiens.

XX Key Location/Qualifiers

FT CDS 376..1023

FT /*tag= a

FT /product= "SCN3B"

XX WO2003072751-A2.

XX PN

XX 04-SEP-2003.

XX PD

XX 25-FEB-2003; 2003WO-US006010.

XX PF

XX 25-FEB-2002; 2002US-0359382P.

XX PR

XX (UYVA-) UNIV VANDERBILT.

XX PA

XX George AL, Lossin C;

XX PI

XX WPI; 2003-712725/67.

XX DR P-FSDB; ABR83183.

XX DR

XX Recombinantly expressed sodium channel type 1 alpha subunit, useful in

PT screening for modulators, for treating e.g. epilepsy.

PT

XX Disclosure; Page 145-147; 176pp; English.

XX PS

XX The invention relates to a recombinantly expressed and isolated human

CC SCN3A (sodium channel type 1 alpha-subunit) (I). (I), optionally

CC incorporated into a cell, is used to screen for specific modulators,

CC potentially useful as anticonvulsant, antiepileptic, neuroprotective,

CC analgesic and/or anesthetic agents, e.g. for treating severe myoclonic

CC epilepsy of infancy, stroke, cardiac arrest, hyperkalemic paralysis,

CC motor endplate diseases, hypertension, congestive heart failure and

CC muscular dystrophy also to treat cancer (SCN3A is expressed in prostatic

CC and metastatic cancer cell lines). These activities can also be provided

CC by gene therapy vectors that express (I) or the modulators. The

CC modulators, also antibodies directed against (I), are used to detect

CC sodium channel polypeptides. The present sequence represents a human

CC SCN3B protein encoding cDNA

XX SQ Sequence 1261 BP; 263 A; 365 C; 372 G; 261 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 2,66e-124 Length: 1261

Score: 1124.00 Matches: 215

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 10 Gaps: 0

US-09-977-579A-2 (1-215) x ACF57870 (1-1261)

QY 1 MetProAlaPheAsnArgLeuPheProLeuAlaSerLeuValLeuIleTyrTrpValSer 20
DB 376 ATGCTGCTTCAATAGATTGTTCCCTGGCTTCTCGTGTATCTACTGGTCACT 435
QY 21 ValCysPheProValCysValGluValProSerGluThrGluAlaValGlnGlyAsnPro 40
DB 436 GTCTGCTTCCCTGTGTGTGAAGTGCCTCGAGACGGAGCGGTGCAGGCGCAACCCC 495
QY 41 MetLysLeuArgCysIleSerCysMetLysArgGluValGluAlaThrThrValVal 60
DB 496 ATGAAGCTGCGCTGCATCTCTCGCATGAAGAGAGAGAGGTGGAGCCACACCGTGGT 555
QY 61 GluTrpPheTyrArgProGluGlyGlyAspPheLeuIleTyrGluTyrArgAsnGly 80
DB 556 GAATGGTCTACAGCCCGGCGGTAAAGATTTCCTTATTACGATATCGAATGCG 615
QY 81 HisGlnGluValGluSerProPheGlnGlyArgLeuGlnTrpAsnGlySerLysAspLeu 100

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Db 616 CACCAGGAGTGGAGAGCCCTTTTCAGGGGCGCTCGAGTGAATGGAGCAAGGACCTG 675
Qy 101 GlnAspValSerIleThrValLeuAsnValThrLeuAsnAspSerglyLeuTyrThrCys 120
Db 676 CAGGACGTGTCCATCACTGTGCTCAACGTCACTCTGAACGACTCTGGCCTCTCACCTGC 735
Qy 121 AsnValSerArgGluPheGluAlaHisargProPheValysThrThrArgLeu 140
Db 736 AATGTGTCCTCCGGAGTTTGAGTTTGAGCGCATCGGCCCTTTGTGAAGACACGCGCTG 795
Qy 141 IleProLeuArgValThrGluAlaGlyGluAspPheThrSerValValSerGluIle 160
Db 796 ATCCCTTAAGATCACCAGAGGCTGGAGAGACTTCACCTCTGTGGTCTCAGAATC 855
Qy 161 MetMetTyrIleLeuLeuValPheLeuThrLeuTrpLeuLeuIleGluMetIleTyrCys 180
Db 856 ATGATGTACATCTCTGCTCTCCTCACCTGGCTGTCTCATCGAGATGATATATTC 915
Qy 181 TyrArgLysValSerLysAlaGluAlaGlnGluAsnAlaSerAspTyrLeuAla 200
Db 916 TACAGAAAGGTCTCAAAAGCCGAGAGAGCCCAAGAAACGCGTCTGACTACCTTGCC 975
Qy 201 IleProSerGluAsnLysGluAsnSerAlaValProValGluGlu 215
Db 976 ATCCCATCTGAGACAGAGAACTCTGCGGTACCACTGGAGGAA 1020

RESULT 4
AAF84146
ID AAF84146 standard; cDNA; 1510 BP.
XX
XX AAF84146;
AC
XX 07-SEP-2001 (first entry)
DT
DE Human novel sodium channel betal-like subunit encoding cDNA.
XX
XX Sodium channel; sensory neurone specific channel; betal-like subunit;
KW SNS; therapeutic; pain; analgesic; ss.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 213..860
XX /*tag= a
XX /product= "sodium channel betal-like subunit"
XX
XX WO200144293-A2.
XX
XX 21-JUN-2001.
XX
XX 14-DEC-2000; 2000WO-GB004802.
XX
XX P-PSDB; AAB85206.
XX
XX (GLAX ) GLAXO GROUP LTD.
XX
XX Plumpton M, Powell AJ, Sanseau P;
XX
XX WPI; 2001-398129/42.
XX
XX P-PSDB; AAB85206.
XX
XX Novel sub-unit for voltage-gated sodium channel proteins for producing
XX agents useful for treating pain.
XX
XX Claim 4; Page 29-30; 31pp; English.
XX
XX The invention provides a novel betal-like sub-unit for voltage-gated
XX sodium ion channel polypeptide, specifically a sensory neurone specific
XX channel (SNS) subunit. The novel betal-like subunit is useful for
XX producing a therapeutic agent which is useful treating pain in a patient.
XX The subunit can be expressed by standard recombinant methodology. The
XX present sequence represents a human novel sodium channel betal-like
XX subunit encoding cDNA
```

```
XX SQ Sequence 1510 BP; 350 A; 410 C; 414 G; 336 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 3.43e-124 Length: 1510
Score: 1124.00 Matches: 215
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0
US-09-977-579A-2 (1-215) x AAF84146 (1-1510)
Qy 1 MetProAlaPheAsnArgLeuPheProLeuAlaSerLeuValLeuIleTyrTrpValSer 20
Db 213 ATGCCTCCCTTCAATAGATTGTTTCCCTCGCTTCTCTCGTGTCTATCTACTGGGTCAGT 272
Qy 21 ValCysPheProValCysValGluValProSerGluThrGluAlaValGlnGlyAsnPro 40
Db 273 GTCTGCTTCCCTGTGTGTGTGGAGTCCCTTCGGAGACGAGGCGCTGCAGGGCAACCCC 332
Qy 41 MetLysLeuArgCysIleSerCysMetLysArgGluGluValGluAlaThrThrValVal 60
Db 333 ATGAAGCTGCGCTGCATCTCTGCATCAAGAGAGAGAGGTGGAGGCCACCACCGTGGTG 392
Qy 61 GluTrpPheTyrArgProGluGlyGlyLysAspPheLeuIleTyrGluTyrArgAsnGly 80
Db 393 GAATGGTTCTACAGGCCCGGCGGTAAAGATTCTCTTATTTACGAGTATCGGAATGGC 452
Qy 81 HisGlnGluValGluSerProPheGlnGlyArgLeuGlnTrpAsnGlySerLysAspLeu 100
Db 453 CACCAGAGGTGGAGAGCCCTTTTCAGGGGCGCTGCGATGGATGGCAGCAGGACCTG 512
Qy 101 GlnAspValSerIleThrValLeuAsnValThrLeuAsnAspSerglyLeuTyrThrCys 120
Db 513 CAGGACGTGTCCATCACTGTGCTCAACGTCACTCTGAACGACTCTGGCCTCTACACCTGC 572
Qy 121 AsnValSerArgGluPheGluAlaHisargProPheValysThrThrArgLeu 140
Db 573 AATGTGTCCTCCGGAGTTTGAGTTTGAGCGCATCGGCCCTTTGTGAAGACACGCGCTG 632
Qy 141 IleProLeuArgValThrGluGluAlaGlyGluAspPheThrSerValValSerGluIle 160
Db 633 ATCCCCCTAAGATCACCAGAGGCTGGAGAGACTTCACCTCTGTGGTCTCAGAATC 692
Qy 161 MetMetTyrIleLeuLeuValPheLeuThrLeuTrpLeuLeuIleGluMetIleTyrCys 180
Db 693 ATGATGTACATCTCTGCTCTCTCCTCACCTTGTGGCTGCTCATCGAGATGATATATTC 752
Qy 181 TyrArgLysValSerLysAlaGluAlaGlnGluAsnAlaSerAspTyrLeuAla 200
Db 753 TACAGAAAGGTCTCAAAAGCCGAGAGAGCCCAAGAAACGCGTCTGACTACCTTGCC 812
Qy 201 IleProSerGluAsnLysGluAsnSerAlaValProValGluGlu 215
Db 813 ATCCCATCTGAGACAGAGAACTCTGCGGTACCACTGGAGGAA 857

RESULT 5
ABA93727
ID ABA93727 standard; cDNA; 4052 BP.
XX
XX ABA93727;
AC
XX 30-APR-2002 (first entry)
DT
DE Human signal transduction cDNA clone amy2_2f18.
XX
XX Human; foetal brain; foetal kidney; melanoma; testis; amygdala;
KW gene therapy; ss.
XX
XX Homo sapiens.
XX
XX WO200198454-A2.
XX
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XX PD 27-DEC-2001.
XX PF 25-APR-2001; 2001WO-IB002050.
XX PR 25-APR-2000; 2000US-0199380P.
XX PA (GEHU-) GERMAN HUMAN GENOME PROJECT.
XX PI Wiemann S;
XX WPI; 2002-055860/07.
XX DR P-PSDB; ABB05689.
XX PT Human cDNA sequences and clones derived from human fetal brain, fetal
XX PT kidney, melanoma, testis and amygdala cDNA libraries, useful in genetic
XX PT screening and therapy.
XX PS Claim 1; Page 174-175; 611pp; English.
XX CC The present invention describes assemblies and computer readable media
XX CC comprising novel human cDNA sequences and clones derived from human
XX CC foetal brain, foetal kidney, melanoma, testis and amygdala cDNA
XX CC libraries. ABA93702 to ABA93766 represent human cDNA sequences from the
XX CC present invention which encode the proteins given in ABB05662 to
XX CC ABB05729. The human cDNA sequences and clones can be used in gene
XX CC therapy. The clones may be used in a variety of applications, for example
XX CC they may be used in profiling assays, for providing large arrays of human
XX CC genetic material for implementing large-scale screening strategies and
XX CC for treating diseases via gene therapy procedures
XX SQ Sequence 4052 BP; 994 A; 1033 C; 1036 G; 989 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1.4e-123 Length: 4052
Score: 1124.00 Matches: 215
Percent Similarity: 100.00% Conservativeness: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-977-579A-2 (1-215) x ABA93727 (1-4052)

QY 1 MetProAlaPheAsnArgLeuPheProLeuAlaSerLeuValLeuIleTyrTrpValSer 20
DB 804 ATGCCTGCCTTCAATAGATTGTTCCCTGGCTTCTCTGCTATCTACTGGGTCAGT 863

QY 21 ValCysPheProValCysValGluValProSerGluThrGluAlaValGlnGlyAsnPro 40
DB 864 GTCGTCTCCCTGTGTGTGGAGTGCCTCGGACGCGGCGCTGCAGGCGCAACCC 923

QY 41 MetLysLeuArgCysIleSerCysMetLysArgGluGluValGluAlaThrThrValVal 60
DB 924 ATGAAGCTGGCTGCATCTCTCATGAAGAGAGAGAGGAGGAGGAGGAGGAGGAGGAGG 983

QY 61 GluTrpPheTyrArgProGluGluGlyLysAspPheIleTyrGluTyrArgGly 80
DB 984 GAATGGTTCTACAGGCGCGGCGGTAAGATTCTCTATTATTCAGGATGCGAATGCG 1043

QY 81 HisGlnGluValGluSerProPheGlnGlyArgLeuGlnTrpAsnGlySerLysAspLeu 100
DB 1044 CACGAGAGTGAGAGAGCCCTTTTCAGGCGCGCTCGAGTGGAGTGGCAGCAGGACCTG 1103

QY 101 GlnAspValSerIleThrValLeuAsnValThrLeuAsnAspSerGlyLeuTyrThrCys 120
DB 1104 CAGAGCGTGCATCTACTGTGCTCAAGCTCACTCTGAACGACTCTGGCCTCTACACTGC 1163

QY 121 AsnValSerArgGluPheGluPheGluAlaHisArgProPheValLysThrThrArgLeu 140
DB 1164 AATGTGTCCCGGAGTTTGAGTTTGAGGCGCATCGGCCCTTTGTGAAGACGACGCGGCTG 1223

QY 141 IleProLeuArgValThrGluGluAlaGlyLysAspPheThrSerValValSerGluIle 160

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Db 1224 ATCCCCCTAGAGTCACCGAGGAGGCTGGAGAGACTTACCTCTGGTGTCTCAGAAATC 1283
QY 161 MetMetTyrIleLeuLeuValPheLeuThrLeuTrpLeuLeuIleGluMetIleTyrCys 180
Db 1284 ATGATGTACATCTCTTCTGGTCTTCTACCTTGTGGCTGCTCATCGAGATGATATATTC 1343
QY 181 TyrArgLysValSerLysAlaGluGluAlaGlnGluAlaSerAspTyrLeuAla 200
Db 1344 TACAGAAAGGTCTCAAAAGCCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1403
QY 201 IleProSerGluAsnLysGluAsnSerAlaValProValGluGlu 215
Db 1404 ATCCCATCTGAGAACAGGAGAACTCTGCGGTACCCAGTGGAGGAA 1448

```

RESULT 6

AAC90601

ID AAC90601 standard; cDNA; 645 BP.

XX AC AAC90601;

XX DT 13-MAR-2001 (first entry)

XX DE Rat sodium channel beta3 protein Alrxa94h5 partial coding sequence.

XX KW Rat; sodium channel beta3 protein; Alrxa94h5; pain; sleep disorder;

XX KW neurodegenerative disorder; mood disorder; muscle contraction; ss.

XX OS Rattus sp.

XX PN WO200069912-A1.

XX PD 23-NOV-2000.

XX PF 12-MAY-2000; 2000WO-US013144.

XX PR 14-MAY-1999; 99US-0134198P.

XX PA (MILL-) MILLENNIUM PHARM INC.

XX PI Curtis RAJ;

XX DR WPI; 2001-122743/13.

XX PT New rat sodium channel beta-3 subunit gene isolated from a rat dorsal

XX PT root ganglion cDNA library for use in chromosome mapping, forensic

XX PT medicine, monitoring clinical trials and therapeutics.

XX PS Claim 1; Page 40-41; 145pp; English.

XX CC The present invention provides the protein and coding sequences of the

XX CC rat sodium channel beta3 protein, designated Alrxa94h5. This protein is

XX CC involved in the generation of pain and other sensory or perceptible nerve

XX CC impulses, in the establishment and endurance of mood, neurodegenerative

XX CC and sleep disorders, and in the control of muscle contraction, including

XX CC movements such as the heartbeat, digestion and vascular tone. The

XX CC sequences can be used in predictive medicine, screening and diagnostic

XX CC assays, and in pharmacogenomics

XX SQ Sequence 645 BP; 155 A; 154 C; 181 G; 155 T; 0 U; 0 Other;

```

Alignment Scores:
Pred. No.: 1.93e-122 Length: 645
Score: 1105.00 Matches: 211
Percent Similarity: 98.14% Conservativeness: 0
Best Local Similarity: 98.14% Mismatches: 4
Query Match: 98.31% Indels: 0
DB: 5 Gaps: 0

```

US-09-977-579A-2 (1-215) x AAC90601 (1-645)

QY 1 MetProAlaPheAsnArgLeuPheProLeuAlaSerLeuValLeuIleTyrTrpValSer 20

Db 1 ATGCCTGCCTTCAACAGATTGCTTCCCTAGCTTCTTAGTGTCTACTACTGGGTGAGA 60

Qy 21 ValCysPheProValCysValGluValProSerGluThrGluAlaValGlnGlyAsnPro 40
 Db 61 GTCTGCTTCCCTGTGTGTGGAGTGCCTTCGAGACAGAAAGCGGTGCGAGGCAATCCC 120
 Qy 41 MetLysLeuArgCysIleSerCysMetLysArgGluGluValGluAlaThrThrValVal 60
 Db 121 ATGAAGCTGAGTGCATCTCTCGATGAGAGGAGGAGGTGGAGGCCACCATGTGGTG 180
 Qy 61 GluTrpPheTyrArgProGluGlyGlyAspPheLeuIleTyrGluTyrArgAsnGly 80
 Db 181 GAGTGGTTCACAGCCTCAGGGCGTAAAGATTCTCTATATATGATGATCGGAATGCG 240
 Qy 81 HisGlnGluValGluSerProPheGlnGlyArgLeuGlnTTPAsnGlySerLysAspLeu 100
 Db 241 CACAGGAAGTGGAGAGCCCTTCAGAGCCGCTCGAGTGGAAATGGAGCAAGACCTG 300
 Qy 101 GlnAspValSerIleThrValLeuAsnValThrLeuAsnAspSerGlyLeuTyrThrCys 120
 Db 301 CAGACGTATCCATCATCTACTCAATGTCACTTTGATGACTCTGGCTCTACACATGC 360
 Qy 121 AsnValSerArgGluPheGluPheGluAlaHisArgProPheValLysThrThrArgLeu 140
 Db 361 AATGTGTCAGGGAGTTCGAATTCGAGGCACACAGGCGCTTTGTGAAGACCACGAGACTG 420
 Qy 141 IleProLeuArgValThrGluGluAlaGlyGlyAspPheThrSerValValSerGluIle 160
 Db 421 ATACCTTTGCGAGTCACTGAAGAGCGGAGAGACTTCACCTCCGGTGTCTCGAATC 480
 Qy 161 MetMetTyrIleLeuLeuValPheLeuThrLeuTyrLeuIleGluMetIleTyrCys 180
 Db 481 ATGATGTACATCTCTCTGCTTCTCACCTTGTGGCTGTTATTTGAGATGATCTATTGC 540
 Qy 181 TyrArgLysValSerLysAlaGluGluAlaGlnGlnGluAlaSerAspTyrLeuAla 200
 Db 541 TACAGAAAGGTCTCTAAGAGCGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 600
 Qy 201 IleProSerGluAsnLysGluAsnSerAlaValProValGluGlu 215
 Db 601 ATCCCTTCAGAGAACAGGAGACTCTGTGTGTACCTGTGGAGGAA 645

RESULT 7

ID AAC67836 standard; cDNA; 2220 BP.
 XX
 AC AAC67836;
 XX
 DT 15-FEB-2001 (first entry)
 XX
 DE Rat beta3 subunit cDNA.
 XX
 KW Rat; beta sub-unit; beta3; analgesic; anticonvulsant; cerebroprotective;
 KW vasotrophic; cardiant; nootropic; cytostatic; dermatological;
 KW gene therapy; voltage-gated sodium channel; pain; epilepsy; stroke;
 KW ischaemia; heart disease; Jacobsen Syndrome;
 KW familial nonchromaffin paraganglioma; phenylketonuria;
 KW Charcot Marie Tooth disease; ss.
 XX
 OS Rattus sp.
 XX
 PN W0200063367-Al.
 XX
 PD 26-OCT-2000.
 XX
 XX 24-FEB-2000; 2000WO-EP001783.
 XX
 XX 15-APR-1999; 99US-0129473P.
 XX
 XX (WARN) WARNER LAMBERT CO.
 XX (UYCA-) UNIV CAMBRIDGE TECH SERVICES LTD.
 XX Cox P, Dixon A, Jackson A, Morgan K;
 XX

WPI; 2000-665241/64.

DR P-PSDB; AAB36001.

XX Novel nucleic acids encoding a beta-3 subunit from a voltage-gated sodium channel, and their corresponding polypeptides, useful for detecting and treating sodium channel-associated conditions, e.g. pain, epilepsy and stroke.

XX Claim 6; Page 69-70; 88pp; English.

XX The present sequence is given in the claims of a specification relating to a novel family of beta sub-unit proteins from a voltage-gated sodium channel. Human and rat beta sub-units, which have been collectively identified as beta3, have been isolated. The polynucleotides and polypeptides are useful for screening for agonists and antagonists of sodium channels. The agonists, antagonists, proteins and nucleic acids may be used diagnosing of treating diseases or conditions associated with voltage-gated sodium channels, e.g. pain, epilepsy, stroke, ischaemia, heart disease, Jacobsen Syndrome, Familial Nonchromaffin Paraganglioma, Phenylketonuria and Charcot Marie Tooth disease

XX Sequence 2220 BP; 573 A; 557 C; 561 G; 529 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 1.12e-121 Length: 2220
 Score: 1105.00 Matches: 211
 Percent Similarity: 98.14% Conservatives: 0
 Best Local Similarity: 98.14% Mismatches: 4
 Query Match: 98.31% Indels: 0
 DB: 3 Gaps: 0

US-09-977-579A-2 (1-215) x AAC67836 (1-2220)

Qy 1 MetProAlaPheAsnArgLeuPheProLeuAlaSerLeuValLeuIleTyrTrpValSer 20
 Db 363 ATGCCTCCCTTCAACAGATTGCTTCCCTAGCTTCTCTAGTGTCTCATCTAGTGGT CAGA 422
 Qy 21 ValCysPheProValCysValGluValProSerGluThrGluAlaValGlnGlyAsnPro 40
 Db 423 GTCTGCTTCCCTGTGTGTGGAGTGCCTTCGAGACAGAGGCGGTGCGAGGCAATCCC 482
 Qy 41 MetLysLeuArgCysIleSerCysMetLysArgGluGluValGluAlaThrThrValVal 60
 Db 483 ATGAAGCTGAGTGCATCTCTCGATGAGAGGAGGAGGTGGAGGCCACCATGTGGTG 542
 Qy 61 GluTrpPheTyrArgProGluGlyGlyAspPheLeuIleTyrGluTyrArgAsnGly 80
 Db 543 GAGTGGTTCACAGGCGCTGAGGCGGTAAAGATTCTCTATATGATGATCGGAATGGC 602
 Qy 81 HisGlnGluValGluSerProPheGlnGlyArgLeuGlnTTPAsnGlySerLysAspLeu 100
 Db 603 CACAGGAAGTGGAGAGCCCTTCAGAGCCGCTCGAGTGGAAATGGAGCAAGACCTG 662
 Qy 101 GlnAspValSerIleThrValLeuAsnValThrLeuAsnAspSerGlyLeuTyrThrCys 120
 Db 663 CAGGACGTATCCATCATCTACTCAATGTCACTTTGATGACTCTGGCTCTACACATGC 722
 Qy 121 AsnValSerArgGluPheGluPheGluAlaHisArgProPheValLysThrThrArgLeu 140
 Db 723 AATGTGTCAGGGAGTTCGAATTCGAGGCACACAGGCGCTTTGTGAAGACCACGAGACTG 782
 Qy 141 IleProLeuArgValThrGluGluAlaGlyGlyAspPheThrSerValValSerGluIle 160
 Db 783 ATACCTTTGCGAGTCACTGAAGAGCGGAGAGACTTCACCTCCGGTGTCTCGAATC 842
 Qy 161 MetMetTyrIleLeuLeuValPheLeuThrLeuTyrLeuIleGluMetIleTyrCys 180
 Db 843 ATGATGTACATCTCTCTGCTTCTCACCTTGTGGCTGTTATTTGAGATGATCTATTGC 902
 Qy 181 TyrArgLysValSerLysAlaGluGluAlaGlnGlnGluAlaSerAspTyrLeuAla 200
 Db 903 TACAGAAAGGTCTCTAAGAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 962

CC sequences can be used in predictive medicine, screening and diagnostic
 CC assays, and in pharmacogenomics
 XX SQ Sequence 3108 BP; 830 A; 748 C; 727 G; 803 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1.82e-121 Length: 3108
 Score: 1105.00 Matches: 211
 Percent Similarity: 98.14% Conservative: 0
 Best Local Similarity: 98.14% Mismatches: 4
 Query Match: 98.31% Indels: 0
 DB: 5 Gaps: 0

US-09-977-579A-2 (1-215) x AAC90600 (1-3108)

Qy 1 MetProAlaPheAsnArgLeuPheProLeuAlaSerLeuValLeuIleTyrTrpValSer 20
 Db ATGCGTCGCTTCAACAGATTGCTTCCCTAGCTTCTCTAGTGTCTCATCTACTGGGTGAGA 137
 Qy 21 ValCysPheProValCysValGluValProSerGluThrGluAlaValGlnGlyAsnPro 40
 Db GTCTGCTTCCCTGTGTGTGGAAGTGCCTTCGAGACAGAGCGGTGCGAGGCAATCCC 197
 Qy 41 MetLysLeuArgCysIleSerCysMetLysArgGluValGluAlaThrValVal 60
 Db ATGAAGCTGAGTGCATCTCTCGATGAGAGGAGGAGGTGGAGGCCACCATGTGGTG 257
 Qy 61 GluTrpPheTyrArgProGluGlyGlyLysAspPheLeuIleTyrGluTyrArgAsnGly 80
 Db GAGTGGTTCACAGGCTCAGGCGGTAAAGATTCTCTATATATGAGTATCGGAATGGC 317
 Qy 81 HisGlnGluValGluSerProPheGlnGlyArgLeuGlnTrpAenGlySerLysAspLeu 100
 Db CACAGAGAGTGGAGAGCCCTTCCAAAGCGCGTCTGCAGTGGAAATGGGAGCAAGACTG 377
 Qy 101 GlnAspValSerIleThrValLeuAsnValThrLeuAsnAspSerGlyLeuTyrThrCys 120
 Db CAGAGCTATCCATCATCTACTACTCAATGTCACTTGAATGACTCTGGCTCTACATGC 437
 Qy 121 AsnValSerArgGluPheGluPheGluAlaHisArgProPheValLysThrThrArgLeu 140
 Db AATGTGTCAGGAGTTCGAATTCAGGCACACAGGCGCTTTGTGAAGACACACGAGACTG 497
 Qy 141 IleProLeuArgValThrGluGluAlaGlyGluAspPheThrSerValValSerGluIle 160
 Db ATACCTTTGCGAGTCACTGAAGAGCGGGAAGACTTCACCTCCGTGGTCTCGGAATC 557
 Qy 161 MetMetTyrIleLeuLeuValPheLeuThrLeuTrpLeuLeuIleGluMetIleTyrCys 180
 Db ATGATGTACATCTCTCTGCTTCTCTCACCTTGTGGCTGTTTATTTGAGATGATCTATGC 617
 Qy 181 TyrArgLysValSerLysAlaGluGluAlaGlnGluAsnAlaSerAspTyrLeuAla 200
 Db TACAGAAAGGTCTCTAAGCGCCGAGAGCAGCAGAGGAAATGCGTCTGACTACCTTGGCT 677
 Qy 201 IleProSerGluAenLysGluAsnSerAlaValProValGluGlu 215
 Db ATCCCTTCAGAGAACAGGAGAACTCTGTGTGTTACCTGTGGAGGAA 722

RESULT 10

AAK52345

ID AAK52345 standard; cDNA; 1045 BP.

XX AC AAK52345;

XX DT 06-NOV-2001 (first entry)

XX DE Human polynucleotide SEQ ID NO 890.

XX KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;

KW KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;

KW KW tissue growth factor; immunomodulatory; cancer; leukaemia;

KW KW nervous system disorder; arthritis; inflammation; ss.

XX OS Homo sapiens.
 XX PN WO200157190-A2.
 XX PD 09-AUG-2001.
 XX PF 05-FEB-2001; 2001WO-US004098.
 XX PR 03-FEB-2000; 2000US-00496914.
 XX PR 27-APR-2000; 2000US-00560875.
 XX PR 20-JUN-2000; 2000US-00598075.
 XX PR 19-JUL-2000; 2000US-00620325.
 XX PR 01-SEP-2000; 2000US-00654936.
 XX PR 15-SEP-2000; 2000US-00663561.
 XX PR 20-OCT-2000; 2000US-00693325.
 XX PR 30-NOV-2000; 2000US-00728422.
 XX (HYSE-) HYSEQ INC.
 XX Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y;
 PI Ma Y, Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
 PI Xue AJ, Yang Y, Wejhrman T, Goodrich R;
 XX WPI: 2001-476283/51.
 XX P-PSDB; AAM79212.
 XX Nucleic acids encoding polypeptides with cytokine-like activities, useful
 PT in diagnosis and gene therapy.
 XX Claim 1; Page 2934-2935; 6221pp; English.
 XX The invention relates to polynucleotides (AAK51456-AAK53435) and the
 CC encoded polypeptides (AAM78323-AAM80302) that exhibit activity relating to
 CC cytokine, cell proliferation or cell differentiation or which may induce
 CC production of other cytokines in other cell populations. The
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
 CC peptide therapy. The polypeptides have various cytokine-like activities,
 CC e.g. stem cell growth factor activity, haematopoiesis regulating
 CC activity, tissue growth factor activity, immunomodulatory activity and
 CC activin/inhibin activity and may be useful in the diagnosis and/or
 CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
 CC inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111
 CC (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the
 CC sequence listing were missing at the time of publication
 XX SQ Sequence 1045 BP; 222 A; 289 C; 314 G; 220 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1.96e-112 Length: 1045
 Score: 1024.00 Matches: 195
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 91.10% Indels: 0
 DB: 4 Gaps: 0

US-09-977-579A-2 (1-215) x AAK52345 (1-1045)

Qy 1 MetProAlaPheAsnArgLeuPheProLeuAlaSerLeuValLeuIleTyrTrpValSer 20
 Db ATGCGTCGCTTCAATAGATTGTTTCCCTGGCTTCTCTCGTGTATCTACTCGGTGCTCAGT 361
 Qy 21 ValCysPheProValCysValGluValProSerGluThrGluAlaValGlnGlyAsnPro 40
 Db GTCTGCTTCCCTGTGTGTGGAAGTGCCTTCGAGACGAGGCGGTGCGAGGCAATCCC 421
 Qy 41 MetLysLeuArgCysIleSerCysMetLysArgGluValGluAlaThrValVal 60
 Db ATGAAGCTGCGCTGCATCTCTCGATGAGAGAGAGAGGTGGAGGCCACCATCGTGGTG 481
 Qy 61 GluTrpPheTyrArgProGluGlyGlyLysAspPheLeuIleTyrGluTyrArgAsnGly 80
 Db GAATGGTTCACAGGCCGAGGCGGTAAAGATTCTCTTATTTACGAGTATCGGAATGGC 541

CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 1195 BP; 253 A; 356 C; 381 G; 205 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 8,7e-101 Length: 1195
Score: 927.50 Matches: 184
Percent Similarity: 94.42% Conservative: 2
Best Local Similarity: 93.40% Mismatches: 9
Query Match: 82.52% Indels: 2
DB: 5 Gaps: 1

US-09-977-579A-2 (1-215) x AAS86764 (1-1195)

QY 1 MetProAlaPheAsnArgLeuPheProLeuAlaSerLeuValLeuIleTyrTrpValSer 20
DB 463 ATGCTGCTTCAATAGATTGTTTCCCTGGCTTCTCTCGTCTTATCTACTGAGTCAGT 522

QY 21 ValCysPheProValCysValGlu-ValProSerGluThrGluAla---ValGlnGlyAs 39
DB 523 GTCTGCTTCCCTGTGTGGGGGAAAGTGCCTTAGAAAAACGGGGGGCGGCACGGGCTAA 582

QY 39 nProMetLeuArgCysIleSerCysMetLysArgGluValGluAlaThrThrVa 59
DB 583 CCCCATGAAGCTGCGCTGCATCTCTCTCATGAAGAGAGAGAGTGGAGGCCACACCGGT 642

QY 59 lValGluTrpPheTyrArgProGluGlyGlyLysAspPheLeuIleTyrGluTyrArgAs 79
DB 643 GTTGAATGTTCTACAGCCCGAGGCGGTAAAGATTTCCTTATTACGAGTATCGGA 702

QY 79 nGlyHisGlnGluValGluSerProPheGlnGlyArgLeuGlnTrpAsnGlySerLysAs 99
DB 703 TGGCCACACGAGGAGTGGAGAGCCCTTTTCAGGGGGCGCTGCAGTGGAAATGGCAGCAAGGA 762

QY 99 pleuGlnAspValSerIleThrValLeuAsnValThrLeuAsnAspSerGlyLeuTyrTh 119
DB 763 CTGTGAGGACGTGTGCATCCTCACTGTCTCAACGTCACTCTGAACGACTCTGGCTCTACAC 822

QY 119 rCysAsnValSerArgGluPheGluAlaHisArgProPheValLysThrThrAr 139
DB 823 CTGCAATGTGTCGGGAGTTTGAAGTTCAGGGCGCATCGCCCTTTGTAAGACGACGCG 882

QY 139 gleuIleProLeuArgValThrGluGluAlaGlyLeuAspPheThrSerValValSerGl 159
DB 883 GCTGATCCCTTAAGAGTCAACGAGGAGCTGAGAGGAGTTCACCTCTGTGTGCTCTCAGA 942

QY 159 uileMetMetTyrIleLeuLeuValPheLeuThrLeuTrpLeuLeuIleGluMetIleTy 179
DB 943 AATCATGATGTATCATCTTCTGTGTCTCTCACTTGTCTCACTTGTGTGTCTCATCGAGATGATATA 1002

QY 179 rCysTyrArgLysValSerLysAlaGluGluAlaAlaGlnGluAsnAla 195
DB 1003 TTGCTACACACAGGTCTCAAAAGCCGAGAGGAGCCCAAGAAACGCG 1051

RESULT 14
ADS10151
ID ADS10151 standard; DNA; 953 BP.
XX
AC ADS10151;
XX
XX
DT 16-DEC-2004 (first entry)
XX
DE Human therapeutic DNA - SEQ ID 388.
XX
KW antiinflammatory; neuroprotective; antianaemic; cytostatic; vulnerary;
KW inflammatory; haematopoiesis; immunity; neurodegenerative; stem cell;
KW aplastic anaemia; cancer; wound healing; gene therapy; ds; gené.
XX
OS Homo sapiens.
XX
FN WO2004080148-A2.

XX 23-SEP-2004.
PD
XX
XX 30-SEP-2003; 2003WO-US030720.
PF
XX
XX 02-OCT-2002; 2002US-0416186P.
PR
XX
XX (NUVE-) NUVELO INC.
PA
XX
XX Tang YT, Asundi V, Ren F, Zhang J, Zhang J, Wehrman T, Wang Z, Ma Y; Zhou P;
PI Wang D, Chen R, Zhao QA, Wang J, Ghosh M, Xue AJ, Weng G, Zhou P;
PI
XX
XX WPI; 2004-668857/65.
DR
XX
XX P-PSDB; ADS10835.
XX
XX New polynucleotide, useful in preparing a composition for diagnosing or
PT treating inflammatory, neurodegenerative or stem cell disorders, e.g.,
PT aplastic anemia or cancer for promoting wound healing.
PT
XX
XX Claim 1; SEQ ID NO 388; 718pp; English.
PS
XX
XX The invention relates to a novel isolated polynucleotide and the encoded
CC polypeptide. The molecules of the invention demonstrate antiinflammatory,
CC neuroprotective, antianaemic, cytostatic and vulnerary activities and may
CC be useful in preparing a composition for diagnosing or treating
CC inflammatory, haematopoietic, immune, neurodegenerative or stem cell
CC disorders, such as aplastic anaemia or cancer, as well as for promoting
CC wound healing. The molecules may also be utilised during gene therapy
CC procedures. The current sequence is that of a human therapeutic DNA of
CC the invention. The current sequence is not shown explicitly within the
CC specification but can be accessed from the WIPO web-site.
CC
XX
SQ Sequence 953 BP; 180 A; 279 C; 290 G; 204 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 5,16e-96 Length: 953
Score: 886.50 Matches: 174
Percent Similarity: 84.91% Conservative: 6
Best Local Similarity: 82.08% Mismatches: 19
Query Match: 78.87% Indels: 13
DB: 1 Gaps: 1

US-09-977-579A-2 (1-215) x ADS10151 (1-953)

QY 1 MetProAlaPheAsnArgLeuPheProLeuAlaSerLeuValLeuIleTyrTrpValSer 20
DB 327 ATGCTGCTTCAATAGATTGTTTCCCTGGCTTCTCTCGTCTTATCTACTGGGTCACT 386

QY 21 ValCysPheProValCysValGluValProSerGluThrGluAlaValGlnGlyAsnPro 40
DB 387 GTCTGCTTCCCTGTGTGTGGAAGTGCCTCGAGACGAGGCGCTGCAGGGCAACCCC 446

QY 41 MetLysLeuArgCysIleSerCysMetLysArgGluGluValGluAlaThrThrValVal 60
DB 447 ATGAAGCTGCGCTGCATCTCTTCATGAAGAGAGAGAGTGGAGGCCACCCAGGTGGTG 506

QY 61 GluTrpPheTyrArgProGluGlyGlyLysAspPheLeuIleTyrGluTyrArgAsnGly 80
DB 507 GAATGGTCTTACAGGCCCGAGGCGGTAAAGATTTCCTTATTACGAGTATCGAATGCG 566

QY 81 HisGlnGluValGluSerProPheGlnGlyArgLeuGlnTrpAsnGlySerLysAspLeu 100
DB 567 CACGAGGAGTGGAGAGCCCTTTTCAGGGGGCGCTGCAGTGGAAATGGCAGCAAGGACCTG 626

QY 101 GlnAspValSerIleThrValLeuAsnValThrLeuAsnAspSerGlyLeuTyrThrCys 120
DB 627 CAGGACGTGTCCATCCTGCTCAACGTCACCTCTGAACGACTCTGGCCCTCTACACCTGC 686

QY 121 AsnValSerArgGluPheGluAlaHisArgProPheValLysThrThrArgLeu 140
DB 687 AATGTGTCCCGGAGTTTGTGAGGCGCATTCGCCCTTTGTGAGAGCAGCGCGGCTG 746

QY 141 IleProLeuArgValThrGluGluAlaGlyGluAppPheThrSerValValSerGluIle 160

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Db 747 ATCCCTTAAGAGTCAACGAGGCTGGAGAGGACTTACCTCTGTGGTCTAAACACTTC 806
Qy 151 MetMetTyrIleLeuLeuValPheLeuThrLeuTrpLeuLeuGluMetIleTyrCys 180
Db 807 ATGATGTACATCCTTCTGTGGTGTCTCCACCTT----- 839
Qy 181 TyrArgLysValSerLysAlaGluGluAlaGlnGluAsnAlaSerAspTyrLeuAla 200
Db 840 -----GTGAACCAAGCGCAGCTGCTCCAGAGCACTAGTGTCTCCACAGT 887
Qy 201 IleProSerGluAsnLysGluAsnSerAlaValPro 212
Db 888 GCTCTGATAGTCATCTGGGCTTCCAGCCATCCT 923

RESULT 15
ID AAV86895 standard; cDNA; 471 BP.
AC AAV86895;
XX
XX 27-APR-1999 (first entry)
DE EST clone BM4.
KW Expressed sequence tag; secreted protein; haematopoiesis regulator;
KW tissue growth; activin; inhibin; tumour invasion suppressor; EST; human;
KW chemotaxis; chemokinesis; haemostasis; gene therapy; thrombolysis;
KW receptor; ligand; anti-inflammatory; tumour inhibitor; ds.
XX
OS Homo sapiens.
XX
XX WO9845435-A2.
XX
XX 15-OCT-1998.
XX
XX 10-APR-1998; 98WO-0006954.
XX
XX 10-APR-1997; 97US-00835913.
XX
XX (GEMY ) GENETICS INST INC.
XX
XX Jacobs K, McCoy JM, Lavallie ER, Racie LA, Merberg D, Treacy M;
XX Spaulding V, Agostino MJ;
XX WPI; 1999-070076/06.
XX
XX New polynucleotides encoding human secreted proteins - derived from e.g.
XX human blood, kidney, foetal lung, placenta, testes, brain, ovary,
XX pituitary, retina and colon cDNA libraries.
XX
XX Claim 1; Page 383-384; 633pp; English.
XX
XX This sequence represents an expressed sequence tag (EST), and is a
XX polynucleotide of the invention. The polynucleotides of the invention are
XX all secreted EST sequences isolated from a variety of human tissue
XX sources. The EST sequences and proteins encoded by them are predicted to
XX have useful biological activities which would make them suitable for
XX treating, preventing or ameliorating medical conditions in humans and
XX animals, although no supporting data is given. Suggested activities
XX include nutritional activity, immune stimulating or suppressing activity,
XX haematopoiesis regulating activity, tissue growth activity,
XX activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
XX and thrombolytic activity, receptor/ligand activity, anti-inflammatory
XX activity, cadherin/tumour invasion suppressor activity, tumour inhibition
XX activity. The EST sequences are also stated to be useful for gene therapy
XX
XX Sequence 471 BP; 93 A; 126 C; 143 G; 108 T; 0 U; 1 Other;
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Alignment Scores:

Pred. No.:	3.92e-79	Length:	471
Score:	742.00	Matches:	143
Percent Similarity:	98.62%	Conservative:	0

Best Local Similarity:	98.62%	Mismatches:	2
Query Match:	66.01%	Indels:	1
DB:	2	Gaps:	0
US-09-977-579A-2 (1-215) x AAV86895 (1-471)			
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Qy	21	ValCysPheProValCysValGluValProSerGluThrGluAlaValGlnGlyAsnPro	40
Db	89	GTCTGCTTCCCTGTGTGTGAAGTCCCTCGAGACGGAGCC-GTGCANGGCAACCCC	147
Qy	41	MetLysLeuArgCysIleSerCysMetLysArgGluGluValGluAlaThrThrValVal	60
Db	148	ATGAAGCTGCGCTGCATCTCTGCATGAAGAGAGAGGAGGTGGAGGCCACACGGTGGTG	207
Qy	61	GluTrpPheTyrArgProGluGlyGlyLysAspPheLeuIleTyrGluTyrArgAsnGly	80
Db	208	GAATGGTTCTACAGGCCCGGCGGTAAAGATTTCCTTATTACGAGTATCGGAATGGC	267
Qy	81	HieGlnGluValGluSerProPheGlnGlyArgLeuGlnTrpAsnGlySerLysAspLeu	100
Db	268	CACCAGAGGTGGAGAGCCCTTTACGGGCGCTGCAGTGAATGGCAGCAGGACCTG	327
Qy	101	GlnAspValSerIleThrValLeuAsnValThrLeuAsnAspSerGlyLeuTyrThrCys	120
Db	328	CAGACGTGTCCATCACTGTGCTCAACGTCACTGTGAACGACTCTGGCCTCTACACCTGC	387
Qy	121	AsnValSerArgGluPheGluPheGluAlaHisArgProPheValLysThrThrArgLeu	140
Db	388	AAATGTGTCGGGAGTTTGAGTTTGAGCCGATCGGCCCTTTGTGAAGACGACGGGCTG	447
Qy	141	IleProLeuArgVal 145	
Db	448	ATCCCCCTAAAGATC 462	

Search completed: January 5, 2006, 19:21:05

Job time : 595 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: January 5, 2006, 17:51:34 ; Search time 3869 Seconds

(without alignment)
2599.954 Million cell updates/sec

Title: US-09-977-579A-2

Perfect score: 1124

Sequence: 1 MPANRLPPLASLVIYWS.....SDYLAIPSENKENSAPVVEE 215

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-O=/cgn2.1/USPTO.spool/US0997579/runat_05012006_160653_29024/app_query.fasta_1.391
-DB=EST -QFMT=fastap -SUFFIX=rst -MINMATCH=0.1 -LCOOPEXT=0 -LCOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US0997579 @CGN_1_1 5315 @runat_05012006_160653_29024 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_hc3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_est7:*
9: gb_gsal:*
10: gb_gsal2:*
11: gb_gsal3:*

pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1124	100.0	648	AY419145	AY419145 Homo sapi
2	1124	100.0	2555	CR609664	CR609664 Homo sapi
3	1124	100.0	4052	4 HSM801563	4 HSM801563 Homo sapi
4	1115	99.2	1062	5 BX420015	5 BX420015 Homo sapi
5	1097	97.6	648	10 AY419147	10 AY419147 Mus muscu
6	1097	97.6	1359	4 AK076466	4 AK076466 Mus muscu
7	1097	97.6	3549	4 AK049747	4 AK049747 Mus muscu

8	1084	96.4	4149	4	AK049286	AK049286 Mus muscu
9	1063	94.6	636	3	BM933157	BM933157 UI-M-BH3-
10	1061	94.4	975	5	BX445002	BX445002 BX445002
11	1051	93.5	672	2	BB614118	BB614118 BB614118
12	1042.5	92.7	4105	4	EC058083	EC058083 Mus muscu
13	977	86.9	950	2	BG294174	BG294174 602391245
14	962	85.6	582	3	BP200910	BP200910 BP200910
15	937	83.4	723	6	CA749311	CA749311 UI-M-FY0-
16	927	82.5	629	8	DR003729	DR003729 TC113490
17	868.5	77.3	927	5	BQ713131	BQ713131 AGENCOURT
18	818	72.8	584	3	BP361278	BP361278 BP361278
19	809	72.0	986	5	BUI18914	BUI18914 603142291
20	792	70.5	692	7	CN219870	CN219870 WLA010808
21	788.5	70.2	825	5	BQ745919	BQ745919 UI-M-EX0-
22	774.5	68.9	846	6	CD355879	CD355879 UI-M-FY0-
23	760	67.6	700	3	BI739617	BI739617 603361873
24	747	66.5	582	3	BP311484	BP311484 BP311484
25	747	66.5	892	5	BUI68614	BUI68614 603790206
26	745	66.3	742	6	CB526211	CB526211 UI-M-FY0-
27	744	66.2	595	5	BUI368531	BUI368531 603788820
28	737	65.6	895	5	BX743834	BX743834 BX743834
29	726	64.6	823	8	CX404153	CX404153 JGI_X2T35
30	725	64.5	821	8	CX852822	CX852822 JGI_CAA09
31	718	63.9	584	10	AY419146	AY419146 Pan_trog1
32	701	62.4	845	6	CA327438	CA327438 UI-M-FY0-
33	686.5	61.1	801	8	CX850711	CX850711 JGI_CAA07
34	683	60.8	652	2	BB652801	BB652801 BB652801
35	681	60.6	798	6	CF290312	CF290312 AGENCOURT
36	667.5	59.4	1069	3	BM928131	BM928131 AGENCOURT
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38	622	55.3	734	7	CK367344	CK367344 AGENCOURT
39	618	55.0	823	7	CO428886	CO428886 UI-M-HX0-
40	606	53.9	712	6	CB526257	CB526257 UI-M-FY0-
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42	583	51.9	780	5	BQ770528	BQ770528 UI-M-FY0-
43	582	51.8	750	6	CD349206	CD349206 UI-M-FY0-
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ALIGNMENTS

AY419145 Homo sapiens HCM6793 gene, VIRTUAL TRANSCRIPT, partial sequence, 648 bp DNA linear GSS 12-DEC-2003
AY419145 genomic survey sequence.

AY419145.1 GI:39775105

GSS.

Homo sapiens (human)

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo.

1 (bases 1 to 648)

Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarawal, A.,

Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,

Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,

Adams, M.D. and Cargill, M.

Inferred nonneutral evolution from human-chimp-mouse orthologous

gene trios

Science 302 (5652), 1960-1963 (2003)

2 (bases 1 to 648)

Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarawal, A.,

Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,

Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,

Adams, M.D. and Cargill, M.

Direct Submission

Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,

Rockville, MD 20850, USA

These sequences were made by sequencing genomic exons and ordering

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them based on alignment.
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Score:                100.00%      Conservative: 0
Percent Similarity:   100.00%      Mismatches:  0
Best Local Similarity: 100.00%      Indels:      0
Query Match:         100.00%      Gaps:        0
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Qy  21 ValCysPheProValCysValGluValProSerGluThrGluAlaValGlnGlyAsnPro 40
Db  61 GTCTGCTTCCCTGTGTGTGGAAGTGCCTTCGGAGACGGAGGCCGTGCGAGGGCAACCCC 120
Qy  41 MetLysLeuArgCysIleSerCysMetLysArgGluGluValGluAlaThrThrValVal 60
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Qy  61 GluTrpPheTyrArgProGluGlyGlyLysAspPheLeuIleTyrGluTyrArgAsnGly 80
Db  181 GAATGGTTCTACAGCCCGAGGGCGGTAAAGATTTCCTTATTACGAGTATCGGAATGCG 240
Qy  81 HisGlnGluValGluSerProPheGlnGlyArgLeuGlnTrpAsnGlySerLysAspLeu 100
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Qy  101 GlnAspValSerIleThrValLeuAsnValThrLeuAsnAspSerGlyLeuTyrThrCys 120
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Qy  181 TyrArgLysValSerLysAlaGluGluAlaGlnGluAsnAlaSerAspTyrLeuAla 200
Db  541 TACAGAAAGGTCTCAAAAGCGCAAGAGCGACGCCCAAGAAACCGCTCTGACTACCTTGGC 600
Qy  201 IleProSerGluAsnLysGluAsnSerAlaValProValGluGlu 215
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RESULT 2
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LOCUS             CR609664             2555 bp      mRNA      linear      HTC 21-JUL-2004
DEFINITION       full-length cDNA clone CS0DF023YA09 of Fetal brain of Homo sapiens
                 (human).
ACCESSION       CR609664
VERSION         CR609664.1      GI:50490471
KEYWORDS        HTC;  CNSLT. cDNA.
SOURCE          Homo sapiens (human)

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ORGANISM          Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE         1 (bases 1 to 2555)
AUTHORS           Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE             Full-length cDNA libraries and normalization
JOURNAL           Unpublished
REMARK            Contact : feng liang Email : fliang@lifetech.com URL :
                  http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
                  Faraday Avenue
REFERENCE         2 (bases 1 to 2555)
AUTHORS           Genoscope.
TITLE             Direct Submission
JOURNAL           Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
                  BP 191 91006 EVRY cedex - FRANCE (E-mail : segret@genoscope.cns.fr)
                  - Web : www.genoscope.cns.fr)
COMMENT           1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
                  end enriched, double-strand cDNA was digested with Not I and cloned
                  into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
                  was normalized. Library was constructed by Life Technologies, a
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Query Match:      100.00%      Gaps:        0
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Qy  61 GluTrpPheTyrArgProGluGlyGlyLysAspPheLeuIleTyrGluTyrArgAsnGly 80
Db  415 GAATGGTTCTACAGGCCCGGAGGCGGTAAAGATTTCCTTATTACGAGTATCGGAATGCG 474
Qy  81 HisGlnGluValGluSerProPheGlnGlyArgLeuGlnTrpAsnGlySerLysAspLeu 100
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Db  595 AATGTGTCCCGGAGTTGAGTTTGGGCGCATCGGCCCTTTTGTGAAGACGACGCGGCTG 654
Qy  141 IleProLeuArgValThrGluGluAlaGlyLysAspPheThrSerValValSerGluIle 160
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181 TyrArgLysValSerLysAlaGluGluAlaAlaGlnGluAenAlaSerAspTyrLeuAla 200
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835 ATCCCATCTGAGAACAGAGAACTCTGCGGTACCAAGTGGAGGAA 879

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ACCESSION AL136589
VERSION AL136589.1 GI:13276680
KEYWORDS HTC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 4052)
Ottewaelder,B.; Obermaier,B., Deutschenbaur,S., Schaiipp,A.,
Mewes,H.W., Weil,B., Amid,C., Osanger,A., Fobo,G., Han,M. and
Wiemann,S.
The German cDNA Consortium
Direct Submission
Submitted (22-SEP-2004) MIPS, Ingolstaedter Landstr.1, D-85764
Neuherberg, GERMANY
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by Medigenomix (Martinsried/Germany) within the cDNA
sequencing consortium of the German Genome Project.
This clone (DKFZp761F182) is available at the RZPD Deutsches
Ressourcenzentrum fuer Genomforschung GmbH in Berlin, Germany.
Please contact RZPD for ordering:
http://www.rzpd.de/cgi-bin/products/cl.cgi?cloneID=DKFZp761F182
Further information about the clone and the sequencing project is
available at http://mips.gsf.de/projects/cdna/.

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gene
CDS
REFERENCE
AUTHORS
CONSRTH
TITLE
JOURNAL
COMMENT
REFERENCES
REFERENCES
Li W.B., Gruber C., Jessee J. and Polayes D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On May 13, 2003 this sequence version replaced gi:30646738.
Contact: Genoscope
Genoscope - Centre National de Sequencage

REFERENCES
1 (bases 1 to 1062)
Li W.B., Gruber C., Jessee J. and Polayes D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On May 13, 2003 this sequence version replaced gi:30646738.
Contact: Genoscope
Genoscope - Centre National de Sequencage

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Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
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Qy 21 ValCysPheProValCysValGluValProSerGluThrGluAlaValGlnGlyAenPro 40
Db 864 GTCTGCTTCCCTGTGTGTGGAGTGCCTCGAGAGCGGAGCGGTGCGAGGCAACCC 923
Qy 41 MetLysLeuArgCysIleSerCysMetLysArgGluValGluAlaThrValVal 60
Db 924 ATGAAGCTGGCGTGCATCTCCTGCATGAAGAGAGAGAGGTGGAGGCCACCACCGTGTG 983
Qy 61 GluTrrPheTyrArgProGluGlyLysAspPheLeuIleTyrGluTyrArgAenGly 80
Db 984 GAATGGTCTTACAGCCCGGAGCGGTAAAGATTTCTTATTTACGAGTATCGGAATGCG 1043
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Qy 121 AsnValSerArgGluPheGluPheGluAlaHisArgProPheValLysThrArgLeu 140
Db 1164 AATGTGTCCCGGAGTTGAGTTTGAGCGCATCGGCCCTTTGTGAACACGACCGCGGTG 1223
Qy 141 IleProLeuArgValThrGluGluAlaGlyGluAspPheThrSerValValSerGluLe 160
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Qy 161 MetMetTyrIleLeuLeuValPheLeuThrIleuTrrLeuLeuIleGluMetIleTyrCys 180
Db 1284 ATGATGTACATCTTCTGCTTCTCCTACCTTGTGGTGTCTCATCGAGATGATATATTGC 1343
Qy 181 TyrArgLysValSerLysAlaGluGluAlaAlaGlnGluAenAlaSerAspTyrLeuAla 200
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Qy 201 IleProSerGluAenLysGluAenSerAlaValProValGluGlu 215
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RESULT 4
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LOCUS BX420015 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone
DEFINITION CS0DF023YA09 5-PRIME, mRNA sequence.
ACCESSION BX420015
VERSION BX420015.2 GI:46929710
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 1062)
Li W.B., Gruber C., Jessee J. and Polayes D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On May 13, 2003 this sequence version replaced gi:30646738.
Contact: Genoscope
Genoscope - Centre National de Sequencage

```

2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
 Email: seque@genoscope.cns.fr, Web : www.genoscope.cns.fr
 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
 end enriched, double-strand cDNA was digested with Not I and cloned
 into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
 was not normalized. Library was constructed by Life Technologies, a
 division of Invitrogen.

This sequence belongs to sequence cluster 6147.1

For more information about this cluster, see
<http://www.genoscope.cns.fr/cdna?s=CS0DF023AA05QP1&c=6147.1>.

FEATURES

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 /note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
 was primed with a NotI-oligo(dT) primer. Five prime end
 enriched, double-strand cDNA was digested with Not I and
 cloned into the Not I and EcoRV sites of the pCMVSPORT 6
 vector. Library was not normalized."
 ORIGIN

Alignment Scores:

Pred. No.: 6.51e-125 Length: 1062
 Score: 1115.00 Matches: 214
 Percent Similarity: 99.53% Conservative: 0
 Best Local Similarity: 99.53% Mismatches: 1
 Query Match: 99.20% Indels: 0
 DB: 5 Gaps: 0

US-09-977-579A-2 (1-215) x BX420015 (1-1062)

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 Db 234 ATGCTGCTTCAATAGATTGTTCCCTGCGCTTCTCTCGTGTATCTACTGCGGTGAGT 293

Qy 21 ValCysPheProValCysValGluValProSerGluThrGluAlaValGlnGlyAsnPro 40
 Db 294 GTCTGCTTCCCTGTGTGTGAAGTCCCTCGAGCGAGGCGGTGCAGGGCAACCCC 353

Qy 41 MetLysLeuArgCysIleSerCysMetLysArgGluGluValGluAlaThrValVal 60
 Db 354 ATGAAGCTGCGCTGCTCTCTGCTGAAGAGAGAGAGAGGTGGAGGCCACCCGCTGTG 413

Qy 61 GluTrpPheTyrArgProGluGlyGlyLysAspPheLeuIleTyrGluTyrArgAsnGly 80
 Db 414 GAATGGTTCACAGGCCCGAGGCGGTAAAGATTTCCTTATTTACGAGTATCGGAATGGC 473

Qy 81 HisGlnGluValGluSerProPheGlnGlyArgLeuGlnTrpAsnGlySerLysAspLeu 100
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Qy 101 GlnAspValSerIleThrValLeuAsnValThrLeuAsnAspSerGlyLeuTyrThrCys 120
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Qy 121 AsnValSerArgGluPheGluPheGluAlaHisArgProPheValLysThrArgLeu 140
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Qy 181 TyrArgLysValSerLysAlaGluAlaAlaGlnGluAsnAlaSerAspTyrLeuAla 200

Db 774 TACAGAAGGTCTCAAAAGCGGAGAGGCGCCCAAGAAACGGGTCTGACTACTTGGCC 833

Qy 201 IleProSerGluAsnLysGluAsnSerAlaValProValGluGlu 215
 Db 834 ATCSCATCTGAGAACAAAGGAGAACTCTGCGGTACCACTGAGGAGAA 878

RESULT 5
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 genomic survey sequence.
 ACCESSION AY419147
 VERSION AY419147.1 GI:39775107
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muroidea; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 648)
 AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
 Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
 Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
 Adams,M.D. and Cargill,M.
 TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
 gene trios
 JOURNAL Science 302 (5652), 1960-1963 (2003)
 PUBMED 14671302
 REFERENCE 2 (bases 1 to 648)
 AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
 Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
 Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
 Adams,M.D. and Cargill,M.
 TITLE Direct Submission
 JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
 Rockville, MD 20850, USA
 COMMENT These sequences were made by sequencing genomic exons and ordering
 them based on alignment.
 FEATURES
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 /mol_type="genomic DNA"
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 ORIGIN

Alignment Scores:
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 Score: 1097.00 Matches: 210
 Percent Similarity: 97.67% Conservative: 0
 Best Local Similarity: 97.67% Mismatches: 5
 Query Match: 97.60% Indels: 0
 DB: 10 Gaps: 0

US-09-977-579A-2 (1-215) x AY419147 (1-648)

Qy 1 MetProAlaPheAnArgLeuPheProLeuAlaSerLeuValLeuIleTyrTrpValSer 20
 Db 1 ATGCTGCTTCAACAGATTGCTCCCTAGCTTCTCTAGTCTCATCTACTGCGGTGAGA 60

Qy 21 ValCysPheProValCysValGluValProSerGluThrGluAlaValGlnGlyAsnPro 40
 Db 61 GTCTGCTTCCCTGTGTGTGTAAGTACCCCTCGAGACAGAACCGGTGCAGGCAATTC 120

Qy 41 MetLysLeuArgCysIleSerCysMetLysArgGluGluValGluAlaThrThrValVal 60
 Db 121 ATGAAGCTGAGATGCATCTCTGTCATGAAGAGGAGGTGGAGGCCACCATCTAGTG 180

Qy 61 GluTrpPheTyrArgProGluGlyGlyLysAspPheLeuIleTyrGluTyrArgAsnGly 80
 Db 181 GAGTGGTTCACAGCCCTGAGGCGGTAAAGATTTCCTTATATGATGATGCGAAATGCC 240

Qy	81	HisGlnGluValGluSerProPheGlnGlyArgLeuGlnTrpAsnGlySerLysAspLeu	100
Db	241	CACAGGAGGTGGAGAGCCCTTCCAAAGTCTGTCAGTGGAAATGGAGCAAGACCTG	300
Qy	101	GlnAspValSerIleThrValLeuAsnValThrLeuAsnAspSerGlyLeuThrCys	120
Db	301	CAGGACGTATCCATCAGTCTTCAATGTCACTCTGAATGACTCTGGCCTCTACACATGT	360
Qy	121	AsnValSerArgGluPheGluAlaHisArgProPheValValThrThrArgLeu	140
Db	361	AATGTGTCCAGGAGATTGAGTTTCGAAGCACACCGGCCCTTTGTGAAGACCACAGACTA	420
Qy	141	IleProLeuArgValThrGluGluAlaGlyGluAspPheThrSerValValSerGluIle	160
Db	421	ATACCCCTGCGAGTCAGTGAAGAGCGGAGAGACTTCACCTCGTGGTCTCGGAATC	480
Qy	161	MetMetTyrIleLeuLeuValPheLeuThrLeuTrpLeuLeuGluMetIleTyrCys	180
Db	481	ATGATGTACATCCCTCGTGGCTTCTCCTCACCTTGTGGCTGTTTATTGAGATGATCTATTGC	540
Qy	181	TyrArgLysValSerLysAlaGluGluAlaGlnGluAenAlaSerAspTyrLeuAla	200
Db	541	TACAGAAAGGTCTCTAAGGCCGAAGAGCGAGCTCAGGAAATGCGTCTGACTACCTTGCT	600
Qy	201	IleProSerGluAsnLysGluAsnSerAlaValProValGluGlu	215
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RESULT 6			
AK076466			
LOCUS	AK076466	1359 bp	mRNA linear HTC 03-APR-2004
DEFINITION	Mus musculus 0 day neonate head cDNA, RIKEN full-length enriched library, clone:4833414B02 product:VOLTAGE-GATED SODIUM CHANNEL BETA-3 SUBUNIT (SODIUM CHANNEL BETA 3 SUBUNIT) homolog [Rattus norvegicus], full insert sequence.		
ACCESSION	AK076466		
VERSION	AK076466.1	GI:26345409	
KEYWORDS	HTC; CAP trapper.		
SOURCE	Mus musculus (house mouse)		
ORGANISM	Mus musculus		
REFERENCE	1 Carninci, P. and Hayashizaki, Y. High-efficiency full-length cDNA cloning Meth. Enzymol. 303, 19-44 (1999) 10349636		
AUTHORS	2 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000) 11042159		
TITLE	3 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kishimoto, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000) 11076861		
JOURNAL	4 The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium. Functional annotation of a full-length mouse cDNA collection Nature 409, 685-690 (2001)		
PUBMED			
AUTHORS			
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Qy      41  MetLysLeuArgCysIleSerCysMetLysArgGluValGluAlaThrValVal 60
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Qy      61  GluTrpPheTrpArgProGluGlyGlyLysAspPheLeuIleTrpGluTrpArgAsnGly 80
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CHANNEL BETA-3 SUBUNIT (SODIUM CHANNEL BETA 3 SUBUNIT) homolog
[Rattus norvegicus], full insert sequence.
ACCESSION AK049747
VERSION   AK049747.1 GI:26340475
KEYWORDS HTC; CAP trapper.
SOURCE   Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1
AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
TITLE Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.
Normalizaton and subraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
PUBMED 11042159
AUTHORS Sumi, N., Itoh, M., Aizawa, K., Nagao, S., Sasaki, N., Carninci, P.,
Konno, H., Akiyama, J., Nishi, K., Kitagawa, T., Tashiro, H., Itoh, M.,
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,

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Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M.,
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J.,
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)
11076861
4
The RIKEN Genome Exploration Research Group Phase II Team and the
FANTOM Consortium.
Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)
5
The FANTOM Consortium and the RIKEN Genome Exploration Research
Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 3549)
Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,
Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, M.,
Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T.,
Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,
Kato, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,
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Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akaira, S.,
Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,
Muramatsu, M. and Hayashizaki, Y.
Direct Submission
Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp,
URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
Fax:81-45-503-9216)
COMMENT cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site for further details.
URL:http://genome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/
FEATURES             Location/Qualifiers
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CDS

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ORIGIN


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Db      7  ATGCTGCTTCAACAGATTGCTTCCCTAGCTTCTCTAGTGCTCATCTACTGGGTGAGA 66
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Qy      41 MetLysLeuArgCysValLeuSerCysMetLysArgGluGluValGluAlaThrValVal 60
Db      127 ATGAAGCTGAGATGATCTCTCTGATGAAGAGGAGGAGGTGGAGCCACCACTGTAGTG 186
Qy      61 GluTrpPheTyrArgProGluGlyCysLysAspPheLeuLeuLeuLeuLeuLeuLeuLeu 80
Db      187 GAGTGGTTCTACAGGCTGAGGGGTAAGATTTCCTTATATATAGTATCGAAATGGC 246
Qy      81 HisGlnGluValGluSerProPheGlnGlyArgLeuGlnTrpAsnGlySerLysAspLeu 100
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Qy      101 GlnAspValSerIleThrValLeuAsnValThrLeuAsnAspSerGlyLeuTyrThrCys 120
Db      307 CAGGACGTATCCATCACTGTTCTCAATGCTCACTTGAATGACTCTGGGCTCTACACATGT 366
Qy      121 AsnValSerArgGluPheGluAlaHisArgProPheValLysThrArgLeu 140
Db      367 ATGTGTCAGGGAGTTGAGTTCGAAGACACACCGGCCCTTTGTGAAGACCAAGACTA 426
Qy      141 IleProLeuArgValThrGluGluAlaGlyGluAspPheThrSerValValSerGluLeu 160
Db      427 ATACCCCTGCGAGTCACTGAAGAGCGGAGAGACTTCACCTCCGTGGTCTCGGAATC 486
Qy      161 MetMetTyrIleLeuLeuValPheLeuThrLeuTrpLeuLeuLeuLeuLeuLeuLeuLeu 180
Db      487 ATGATGTATACCTCTCTGCTTCTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 546
Qy      181 TyrArgLysValSerLysAlaGluGluAlaGlnGluAsnAlaSerAspTyrLeuAla 200
Db      547 TACGAAGGTTCTTAAGTGTGAAGAGGAGGAGTTCAGGAATGCTGCTGACTACCTTGT 606
Qy      201 IleProSerGluAsnLysGluAsnSer 209
Db      607 ATCCCTTCAGAGAACACAGAGACTCT 633

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RESULT 10
 LOCUS BX445002
 DEFINITION BX445002 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone
 CS0DF023YA09 5-PRIME, mRNA sequence.

ACCESSION BX445002
 VERSION BX445002.2 GI:47009181
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homiidae; Homo.
 1 (bases 1 to 975)
 Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
 Full-length cDNA libraries and normalization
 Unpublished (2001)
 On May 15, 2003 this sequence version replaced gi:30782286.

COMMENT
 Contact: Genoscope
 Genoscope - Centre National de Sequencage
 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
 end enriched, double-strand cDNA was digested with Not I and cloned
 into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
 was not normalized. Library was constructed by Life Technologies, a
 division of Invitrogen.

This sequence belongs to sequence cluster 6147.r
 For more information about this cluster, see
 http://www.genoscope.cns.fr/cdna?8=CSIAF0062E05QP1&c=6147.r.
 Location/Qualifiers

FEATURES

source

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1. 975
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DF023YA09"
/tissue_type="FETAL BRAIN"
/dev_stage="fetal"
/clone_lib="Homo sapiens FETAL BRAIN"
/notes="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-strand cDNA was digested with Not I and
cloned into the Not I and EcoRV sites of the pCMVSPORT 6
vector. Library was not normalized."

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ORIGIN

Alignment Scores:
 Pred. No.: 2,26e-118 Length: 975
 Score: 1061.00 Matches: 209
 Percent Similarity: 97.67% Conservative: 1
 Best Local Similarity: 97.21% Mismatches: 5
 Query Match: 94.40% Indels: 1
 Gaps: 0

US-09-977-579A-2 (1-215) x BX445002 (1-975)

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Qy      1 MetProAlaPheAsnArgLeuPheProLeuAlaSerLeuValLeuLeuLeuLeuLeuLeu 20
Db      235 ATGCTGCTTCAATAGATTGTTTCCCTGCTTCTCTCGTGTATCTACTGGGTGAGT 294
Qy      21 ValCysPheProValCysValGluValProSerGluThrGluAlaValGlnGlyAsnPro 40
Db      295 GTCTGCTTCCCTGTGTGTGAAGTGCCTCGGAGACGAGGCGCTGCAGGGCAACCCC 354
Qy      41 MetLysLeuArgCysIleSerCysMetLysArgGluGluValGluAlaThrThrValVal 60
Db      355 ATGAAGCTGCGCTGCATCTCTGTCATGAAGAGAGAGAGGAGGTGGAGCCACCAACGGTGG 414
Qy      61 GluTrpPheTyrArgProGluGlyCysLysAspPheLeuLeuLeuLeuLeuLeuLeuLeu 80
Db      415 GAATGGTTCTACAGGCCCGAGGGCGGTAAAGATTTCCTTATTACGAGTATCGAATGGC 474
Qy      81 HisGlnGluValGluSerProPheGlnGlyArgLeuGlnTrpAsnGlySerLysAspLeu 100
Db      475 CACGAGGAGGTGGAGAGCCCTTTTCAGGGGCGCTTCGAGTGGAAATGGCAGCAAGACCTG 534
Qy      101 GlnAspValSerIleThrValLeuAsnValThrLeuAsnAspSerGlyLeuTyrThrCys 120
Db      535 CAGGACGTATCCATCACTGCTCAACGTCACTCTGAACGACTCTGGGCTCTACACCAAC 594
Qy      121 AsnValSerArgGluPheGluAlaHisArgProPheValLysThrArgLeu 140
Db      595 AAWAAGTCCCGGAGTTTGTAGTTTTCAGGGCGCATCGGCCCTTTGTGAAGACGACGGGCTG 654
Qy      141 IleProLeuArgValThrGluGluAlaGlyGluAspPheThrSerValValSerGluLeu 160
Db      655 ATCCCCCTAAGAGTCAACGAGGAGGCTGGAGAGGACTTCACCTCTGTGTGCTCTCAGAAATC 714
Qy      161 MetMetTyrIleLeuLeuValPheLeuThrLeuTrpLeuLeuLeuLeuLeuLeuLeuLeu 180
Db      715 ATGATGTATACATCTCTGCTTCTCCTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 774
Qy      181 TyrArgLysValSerLysAlaGluGluAlaGlnGluAsnAlaSerAspTyrLeuAla 200
Db      775 TACGAAGGTTCTTAAGTGTGAAGAGGAGGAGTTCAGGAATGCTGCTGACTACCTTGGC 834
Qy      201 IleProSerGluAsnLysGluAsnSerAlaValProValGluGlu 215
Db      835 ATCCCATCTCAGAACACAGAGGAGAC-TCTGGCGGTAMCAGTGGAGGAT 878

```

RESULT 11
 BB614118
 LOCUS BB614118
 DEFINITION BB614118 RIKEN full-length enriched, 0 day neonate head Mus

BB614118 672 bp mRNA linear EST 26-OCT-2001


```

SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 4105)
AUTHORS    Strausberg, R.L., Feingold, B.A., Grouse, L.H., Derge, J.G.,
            Klausner, R.D., Collins, F.S., Wagner, L.H., Shenmen, C.M., Schuler, G.D.,
            Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
            Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Heide, F.,
            Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
            Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
            Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
            Carninci, P., Prange, C., Raha, S.S., Iqbal, N.A., Peters, G.J.,
            Abramson, R.D., Mullah, S.J., Bosak, S.A., McEwan, P.J.,
            McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
            Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
            Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
            Fahey, J., Helton, E., Kettman, M., Madan, A., Rodriguez, S.,
            Sanchez, A., Whitting, M., Madan, A., Young, A.C., Shvachenko, Y.,
            Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, B.D.,
            Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
            Butlerfield, Y.S., Krzywicki, M.I., Skalska, U., Smalish, D.E.,
            Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
            Generation and initial analysis of more than 15,000 full-length
            human and mouse cDNA sequences
            Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
            12477932
2 (bases 1 to 4105)
AUTHORS    Strausberg, R.
TITLE      Direct Submission
JOURNAL    Submitted (08-SEP-2003) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
REMARK     NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT    Contact: MGC help desk
            Email: cgapbs-remail.nih.gov
            Tissue Procurement: Dr. Jim Lin, University of Iowa
            cDNA Library Preparation: M. Bento Soares, University of Iowa
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Genome Sequence Centre,
            BC Cancer Agency, Vancouver, BC, Canada
            info@bcgsc.bc.ca
            Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,
            Sueanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin,
            Leticia Hailao, Martin Krzywicki, Reta Kutsche, Oliver Lee, Soo
            Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven
            Nese, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline
            Schein, Duane Smalish, Michael Smith, Lorraine Spence, Jeff Stott,
            Michael Thorne, Miranada Tai, Natasja van den Bosch, Jill Vardy,
            George Yang, Scott Zuyderduyn, Marco Marra.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAC Plate: 126 Row: 1 Column: 19
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 23943798
This clone has the following problem: frame shifted.

FEATURES   Location/Qualifiers
            1..4105
            /organism="Mus musculus"
            /mol_type="mRNA"
            /strain="C57BL/6"
            /db_xref="taxon:10090"
            /clone_lib="NIH BMAP_FY0"
            /lab_host="DH10B"
            /notes="Vector: pYX-ASC"

ORIGIN
Alignment Scores:

```

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Pred. No.: 3.21e-115 Length: 4105
Score: 1042.50 Matches: 208
Percent Similarity: 96.74% Conservat: 0
Best Local Similarity: 96.74% Mismatches: 6
Query Match: 92.75% Indels: 3
DB: 4 Gaps: 1

US-09-977-579A-2 (1-215) x BC058083 (1-4105)

Qy 1 MetProAlaPheAanArgLeuPheProLeuAlaSerLeuValLeuLeuTyrTipValSer 20
Db 356 ATGCCTCCCTTCAACAGATGCTTCCCTAGCTTCTCTAGTGCTCATCTACTGGGA---- 411
Qy 21 ValCysPheProValCysValGluValProSerGluThrGluAlaValGlnGlnValAsnPro 40
Db 412 GTCTGCTTCCCTGTGTGTAGAGATACCTCCGAGAGACAGAGCCGTCGAGGCAATTC 471
Qy 41 MetLysLeuArgCysIleSerCysMetLysArgGluGluValGluAlaThrThrValVal 60
Db 472 ATGAAGCTGAGATGCATCTCTCGCATGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 531
Qy 61 GluTrpPheTyrArgProGluGlyGlyLysPhePheLeuLeuTyrGluTyrArgAsnGly 80
Db 532 GAGTGGTTCACAGGCTGAGGCGGTAAGATTTCTTATATATAGATATCGAATTCGAAATG 591
Qy 81 HisGlnGluValGluSerProPheGlnGlyArgLeuGlnTrpAsnGlySerLysAspLeu 100
Db 592 CACAGAGGAGTGGAGAGGCGCTTCAGAGTCTGTGAGTGGAGTGGAGGAGGAGGAGGAG 650
Qy 101 GlnAspValSerIleThrValLeuAsnValThrLeuAsnAspSerGlyLeuTyrThrCys 120
Db 651 CAGGAGCTATCATCTCTCAATGTCTCTCAATGTCTCTCAATGTCTCTCAATGTCTCTCA 710
Qy 121 AsnValSerArgGluPheGluPheGluAlaHisArgProPheValLysThrThrArgLeu 140
Db 711 AATGTGTCCAGGAGTTTGTAGTTGAAGCACACGCGCCCTTTGTGAAGACCAAGACTA 770
Qy 141 IleProLeuArgValThrGluGluAlaGlyGluAspPheThrSerValValSerGluLeu 160
Db 771 ATACCCCTGCGAGTCACTGAGAGAGGCGGAGAGAGACTTCACCTCGGTCTCGGAAATC 830
Qy 161 MetMetTyrIleLeuLeuValPheLeuThrLeuTrpLeuLeuIleGluMetIleTyrCys 180
Db 831 ATGATGTACATCTCTCTGCTCTTCTCACTACCTTGTGGCTGTTTATTTAGATGATCTATT 890
Qy 181 TyrArgLysValSerLysAlaGluGluAlaGlnGluAsnAlaSerAspTyrLeuAla 200
Db 891 TACAGAAAGGCTCTTAAGGCGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 950
Qy 201 IleProSerGluAsnLysGluAsnSerAlaValProValGluGlu 215
Db 951 ATCCCTTCAGAGACACAGAGAGACTCTGTGGTACCGGTGGAGGAA 995

RESULT 13
BG294174 950 bp mRNA linear EST 21-FEB-2001
LOCUS 603391245F1 NIH_MGC_94 Mus musculus cDNA clone IMAGE:4503250 5',
DEFINITION mRNA sequence.
ACCESSION BG294174
VERSION BG294174.1 GI:13054543
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 950)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-remail.nih.gov
            Tissue Procurement: The Cepko Laboratory

```

CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Plate: LLAM10373 Row: i Column: 11
 High quality sequence stop: 643.
 Location/Qualifiers
 1. .950
 /organism="Mus musculus"
 /mol_type="mRNA"
 /db_xref="taxon:10090"
 /clone="IMAGE:4503250"
 /tissue_type="retina"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH_MGC_94"
 /note="Organ: eye; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally; oligo-dT primed. Average insert size 3.3 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH_MGC Library."

FEATURES

source

ORIGIN

Alignment Scores:
 Pred. No.: 3,93e-108 Length: 950
 Score: 977.00 Matches: 198
 Percent Similarity: 93.95% Conservative: 4
 Best Local Similarity: 92.09% Mismatches: 11
 Query Match: 86.92% Indels: 4
 DB: 2 Gaps: 2

US-09-977-579A-2 (1-215) x BG294174 (1-950)

Qy 1 MetProAlaPheAsnArgLeuPheProLeuAlaSerLeuValLeuIleTyrTrpValSer 20
 Db 87 ATGCTGCTTCAACAGATTGTTCCCTAGCTTCTCTAGTGCTCATCTACTGCTGTCAGA 146
 Qy 21 ValCysPheProValCysValGluValProSerGluThrGluAlaValGlnGlyAsnPro 40
 Db 147 GTCTGCTTCCCTGTGTGTAGAAAGTACCCTCGGAGACAGAAAGCCGTGCGAGGCAATTCC 206
 Qy 41 MetLysLeuArgCysIleSerCysMetLysArgGluGluValGluAlaThrValVal 60
 Db 207 ATGAAGCTGAGATCACTCTCTCATGAGAGGAGAGGTGGAGCCACCACTGTAGTG 266
 Qy 61 GluTrpPheTyrArgProGluGlyGlyLysAspPheLeuIleTyrGluTyrArgAsnGly 80
 Db 267 GAGTGGTTCTACAGCCCTGAGGCGGTAAAGATTCTCTATATAGTATCGAAATGGC 326
 Qy 81 HisGlnGluValGluSerProPheGlnGlyArgLeuGlnTrpAsnGlySerLysAspLeu 100
 Db 327 CACCAGAGGTGGAGAGCCCTTCCAGAGTGTCTCGAGTGGAAATGGGAGCAAGACCTG 386
 Qy 101 GlnAspValSerIleThrValLeuAsnValThrLeuAsnAspSerGlyLeuTyrThrCys 120
 Db 387 CAGACGTATCCATCACTGTCTCAATGTCACTCTGAATGACTCTGGCCCTACACATGT 446
 Qy 121 AsnValSerArgGluPheGluAlaHisArgProPheValLysThrThrArgLeu 140
 Db 447 AATGTGTCCAG-GAGTTTGTAGTTCGAAGCACCCGCGCTTTGTGGAAGACCACCAAGACTA 505
 Qy 141 IleProLeuArgValThrGluGluAlaGlyGluAspPheThrSerValValSerGluIle 160
 Db 506 ATACCCCTGCGAGTCACTGAGAGCGGGAGAACTTCACCTCCGTGGTCTCGGAATC 565
 Qy 161 MetMetTyrIleLeuValPheLeuThrLeuTrpLeuLeuIleGluMetIleTyrCys 180
 Db 566 ATGATGTACATCTCTCTGGCTCTCTCACCTTGTGGCTGTTTATGTAGATGATCTATTGC 625
 Qy 181 TyrArgLysValSerLysAlaGluAlaAlaGlnGluAsnAlaSerAspTyrLeuAla 200
 Db 626 TACAGAAAGGTCTCTAAGGCCGGAAGAGGAGT-CAGGAAATAGCGTCTGACTACTTG--- 681

Qy 201 IleProSerGluAsnLysGluAsnSerAlaValProValGluGlu 215
 Db 682 TATCCCTTAGAAGACAGGCAA---CCTGTGTGACCGTGCATAG 723

RESULT 14

BP200910
 LOCUS
 DEFINITION BP200910 Sugano cDNA library, amygdala Homo sapiens cDNA clone
 AMR03894, mRNA sequence.

ACCESSION BP200910

VERSION BP200910.1 GI:52050356

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 582)

AUTHORS Suzuki,Y., Yamashita,R., Shiota,M., Sakakibara,Y., Chiba,J.,

Mizushima-Sugano,J., Nakai,K. and Sugano,S.

TITLE Sequence comparison of human and mouse genes reveals a homologous

block structure in the promoter regions

JOURNAL Genome Res. 14 (9), 1711-1718 (2004)

COMMENT 15342556

Contact: Yutaka Suzuki

Department of Virology

Institute of Medical Science, University of Tokyo

4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan

Email: yusuzuki@ims.u-tokyo.ac.jp.

FEATURES

source

1. 582

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="AMR03894"

/tissue_type="amygdala"

/clone_lib="Sugano cDNA library, amygdala"

ORIGIN

Alignment Scores:
 Pred. No.: 1.32e-106 Length: 582
 Score: 962.00 Matches: 182
 Percent Similarity: 99.45% Conservative: 0
 Best Local Similarity: 99.45% Mismatches: 1
 Query Match: 85.59% Indels: 0
 DB: 3 Gaps: 0

US-09-977-579A-2 (1-215) x BP200910 (1-582)

Qy 2 ProAlaPheAsnArgLeuPheProLeuAlaSerLeuValLeuIleTyrTrpValSerVal 21

Db 34 CCTGCTTCAATAGATTGTTCCCTGGCTTCTCTGCTGTATCTACTGGGTCAAGTGC 93

Qy 22 CysPheProValCysValGluValProSerGluThrGluAlaValGlnGlyAsnProMet 41

Db 94 TGTTTCCCTGTGTGTGGAGTGCCTCGAGAGGAGGCCCTGCGAGGCAACCCCATG 153

Qy 42 LysLeuArgCysIleSerCysMetLysArgGluValGluAlaThrValValGlu 61

Db 154 AAGCTGCGCTGCATCTCTCATGAAGAGAGAGAGGTGGAGGCCACACCGTGGTGA 213

Qy 62 TrpPheTyrArgProGluGlyGlyLysAspPheIleTyrGluTyrArgAsnGlyHis 81

Db 214 TGGTTCTACAGGCCGAGGCGGTAAAGATTCTCTTATTTACGAGTATCGGAATGGCCAC 273

Qy 82 GlnGluValGluSerProPheGlnGlyArgLeuGlnTrpAsnGlySerLysAspLeuGln 101

Db 274 CAGAGGTGGAGAGCCCTTTTCAGGGGCGCTCGAGTGGAAATGGCAGCAAGACCTGCAG 333

Qy 102 AspValSerIleThrValLeuAsnValThrLeuAsnAspSerGlyLeuTyrThrCysAsn 121

Db 334 GAGGTGTCCATCACTGTGTCTCAACGTCACTCTGAACGACTCTGGCCTCTACACCTGCAAT 393

Qy 122 ValSerArgGluPheGluAlaHisArgProPheValLysThrThrArgLeuile 141
 Db 394 GTGTCGGGGAGTTTGAGTTTGAGCGCATCGGCCCTTTGTAAGACACCGCGCTGATC 453
 Qy 142 ProLeuArgValThrGluGluAlaGlyGluAspPheThrSerValSerGluileMet 161
 Db 454 CCCCTAGAGTCCACGAGGAGGCTCGAGAGGACTTCACCTCTGTGGTCTCAGAAATCATG 513
 Qy 162 MetTyrIleLeuLeuValPheLeuThrLeuThrPleuLeuileGluMetIleTyrCysTyr 181
 Db 514 ATGTATACCTCTCTGGTCTATCCTACCTGTGTGGTCTCATCGAGATGATATATGCTTAC 573
 Qy 182 ArgLysVal 184
 Db 574 AGAAAGGTC 582

RESULT 15

CA749311 723 bp mRNA linear EST 09-JUL-2003
 LOCUS UI-M-FY0-cdd-k-17-0-UI-r1 NIH_BMAP_FY0 Mus musculus cDNA clone
 DEFINITION IMAGE:6831594 5', mRNA sequence.

ACCESSION

CA749311
 CA749311.1 GI:25570984

VERSION

EST.
 Mus musculus (house mouse)

KEYWORDS

SOURCE Mus musculus
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 723)
 NIH-MGC <http://mgc.nhl.nih.gov/>
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Dr. Jim Lin, University of Iowa
 cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>

This clone was contributed by the Brain Molecular Anatomy Project
 (BMAP)

Seq primer: pYX-5.

Location/Qualifiers

1..723
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6"
 /db_xref="taxon:10090"
 /clone="IMAGE:6831594"
 /tissue_type="whole brain"
 /dev_stage="embryo 13.5,14.5,16.5,17.5dpc"
 /lab_host="NIH BMAP FY0"
 /clone_lib="NIH BMAP FY0"

/note="Organ: Brain; Vector: pYX-Asc; Site:1: EcoR I;
 Site 2: Not I; The library was constructed according
 Bonaïdo, Lennon and Soares, Genome Research, 6:791-806,
 1996. Denatured RNA was size fractionated on a 1% agarose
 gel. First strand cDNA synthesis was primed with oligo-dT
 primer containing a Not I site. Double strand cDNA was
 size selected according to mRNA size fraction, ligated
 with EcoR I adaptor, digested with NotI and then cloned
 directionally into pYX-Asc vector. The library tag
 sequence located between the Not I site and the polyA tail
 is AGGAGACAG. This library was created for the University
 of Iowa Brain Anatomy Project (BMAP). 'Gene Discovery in the
 Developing Mouse Nervous System', supported by National
 Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
 program coordinator."

FEATURES

source

Alignment Scores:

Pred. No.: 2.03e-103 Length: 723
 Score: 937.00 Matches: 180
 Percent Similarity: 97.30% Conservative: 0
 Best Local Similarity: 97.30% Mismatches: 4
 Query Match: 83.36% Indels: 1
 DB: Gaps: 0

US-09-977-579A-2 (1-215) x CA749311 (1-723)

Qy 1 MetProAlaPheAenArgLeuPheProLeuAlaSerLeuValLeuileTyrTrpValSer 20
 Db 170 ATGCTCTGCTTCAACAGATTGCTTCCCTAGCTTCTTAGTGCTCATCTACTGGGTGAGA 229
 Qy 21 ValCysPheProValCysValGluValProSerGluThrGluAlaValIleGlnGlyAsnPro 40
 Db 230 GTCTGCTTCCCTGTGTGTAGAGTAGTACCTTCGGAGACAGAACCGTCGAGGGCAATTC 289
 Qy 41 MetLysLeuArgCysIleSerCysMetLysArgGluGluValGluAlaThrThrValVal 60
 Db 290 ATGAAGCTGAGATGCATCTCTGCATGAAGAGGAGGAGGTGGAGGCCACCACCTGTAGTG 349
 Qy 61 GluTrpPheTyrArgProGluGlyGlyLysAspPheLeuileTyrGluTyrArgHengly 80
 Db 350 GAGTGGTTCTACAGGCTGTAGGGCGGTAAAGATTCTTATATATATATATATATATATG 409
 Qy 81 HisGlnGluValGluSerProPheGlnGlyArgLeuGlnTrpAsnGlySerLysAspLeu 100
 Db 410 CACCAGGAGGTGGAGAGGCCCTTCAGAGTGTCTGCAGTGGATGGGAGCAAGACCTG 469
 Qy 101 GlnAspValSerIleThrValLeuAsnValThrLeuAsnAspSerGlyLeuTyrThrCys 120
 Db 470 CAGGAGGTATCCATCCTCTCACTCTCACTCTGAATGACTCTGGCTCTACACATGT 529
 Qy 121 AsnValSerArgGluPheGluAlaHisArgProPheValLysThrThrArgLeu 140
 Db 530 AATGTGTCCAGGAGTTTGAGTTCGAAGCACACCGGCCCTTTGTGAAGACCAAGACTA 589
 Qy 141 IleProLeuArgValThrGluGlu-AlaGlyGluAspPheThrSerValValSerGluil 160
 Db 590 ATACCCCTGCGAGTCACCTGAAGAGCGGGAGAGACTTCACCTCGGTGGTCTCGGAAT 649
 Qy 160 eMetMetTyrIleLeuLeuValPheLeuThrLeuThrPleuLeuileGluMetIleTyrCy 180
 Db 650 CATGATGTACATCTCTCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 709
 Qy 180 eTyrArgLysVal 184
 Db 710 CTACAGAAAGGTC 722

Search completed: January 5, 2006, 18:57:59
 Job time : 3888 secs

ORIGIN

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: January 5, 2006, 17:54:56 ; Search time 778 Seconds

(without alignments)
2285.239 Million cell updates/sec

Title: US-09-977-579A-2

Perfect score: 1124

Sequence: 1 MPANRRLPLASLVLIYVWS.....SDYLAIPISENKENSAPVVEE 215

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

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-FGAPOP=6 -FCAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA_Main:

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10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1124	100.0	1261	3	US-09-977-579-4
2	1124	100.0	1261	9	US-10-482-834A-22
3	1105	98.3	645	5	US-10-029-191-21
4	1105	98.3	2220	3	US-09-977-579-3
5	1105	98.3	2632	5	US-10-029-191-22
6	1105	98.3	3108	3	US-10-029-191-1
7	927.5	82.5	1195	9	US-10-450-763-22568
8	694	61.7	3531	9	US-10-450-763-22567
					Sequence 22567, A
					Sequence 22, Appl
					Sequence 21, Appl
					Sequence 22, Appl
					Sequence 1, Appl
					Sequence 22568, A

9	598	53.2	600	10	US-11-060-756-2816	Sequence 2816, Ap
10	598	53.2	600	10	US-11-060-756-2817	Sequence 2817, Ap
11	598	53.2	600	10	US-11-060-756-7088	Sequence 7088, Ap
12	598	53.2	600	10	US-11-060-756-7089	Sequence 7089, Ap
13	477	42.4	657	5	US-10-029-191-23	Sequence 23, Appl
14	473	42.1	1335	8	US-10-723-860-2247	Sequence 2247, Ap
15	473	42.1	1414	8	US-10-477-272-1	Sequence 1, Appl
16	472	42.0	1414	9	US-10-482-834A-11	Sequence 11, Appl
17	472	42.0	1490	3	US-09-917-800A-1654	Sequence 1654, Ap
18	470	41.8	1275	10	US-11-060-756-3901	Sequence 3901, Ap
19	470	41.8	1275	10	US-11-060-756-8173	Sequence 8173, Ap
20	465	41.4	1414	9	US-10-482-834A-12	Sequence 12, Appl
21	408.5	36.3	621	9	US-10-450-763-22566	Sequence 22566, A
22	396.5	35.3	545	4	US-09-925-065A-774904	Sequence 774904, A
23	260.5	23.2	974	6	US-10-401-916-13	Sequence 12, Appl
24	258.5	23.0	807	6	US-10-401-916-12	Sequence 718, Ap
25	234	20.8	407	7	US-10-276-774-718	Sequence 111, Ap
26	167	14.9	1029	7	US-10-205-331-111	Sequence 471, Ap
27	165.5	14.7	3583	8	US-10-723-860-6471	Sequence 6471, Ap
28	163.5	14.5	1929	3	US-09-960-706-472	Sequence 472, App
29	160.5	14.3	970	9	US-10-874-706-84	Sequence 84, Appl
30	160.5	14.3	983	5	US-10-053-107-11	Sequence 11, Appl
31	160.5	14.3	983	5	US-10-227-884-237	Sequence 237, App
32	160.5	14.3	983	5	US-10-230-163-237	Sequence 237, App
33	160.5	14.3	983	5	US-10-230-338-237	Sequence 237, App
34	160.5	14.3	983	5	US-10-218-631-237	Sequence 237, App
35	160.5	14.3	983	5	US-10-230-414-237	Sequence 237, App
36	160.5	14.3	983	5	US-10-213-145-11	Sequence 11, Appl
37	160.5	14.3	983	5	US-10-232-224-237	Sequence 237, App
38	160.5	14.3	983	5	US-10-218-159A-237	Sequence 237, App
39	160.5	14.3	983	5	US-10-218-849-237	Sequence 237, App
40	160.5	14.3	983	5	US-10-227-873-237	Sequence 237, App
41	160.5	14.3	983	5	US-10-227-883-237	Sequence 237, App
42	160.5	14.3	983	5	US-10-219-076-237	Sequence 237, App
43	160.5	14.3	983	5	US-10-230-434-237	Sequence 237, App
44	160.5	14.3	983	5	US-10-213-199-11	Sequence 11, Appl
45	160.5	14.3	983	5	US-10-219-003-237	Sequence 237, Appl

ALIGNMENTS

RESULT 1

US-09-977-579-4

; Sequence 4, Application US/09977579

; Publication No. US20040248240A1

; GENERAL INFORMATION:

; APPLICANT: Cambridge University Technical Services

; TITLE OF INVENTION: A novel family of beta sub-unit proteins from a voltage gated so

; TITLE OF INVENTION: channel

; TITLE OF INVENTION: nucleic acids encoding them and therapeutic or diagnostic uses

; FILE REFERENCE: 674558-2001

; CURRENT APPLICATION NUMBER: US/09/977,579

; CURRENT FILING DATE: 2001-10-15

; PRIOR APPLICATION NUMBER: PCT/EP00/01783

; PRIOR FILING DATE: 2000-02-24

; PRIOR APPLICATION NUMBER: 60,129,473

; PRIOR FILING DATE: 2000-02-24

; NUMBER OF SEQ ID NOS: 47

; SOFTWARE: Patentin version 3.1

; SEQ ID NO 4

; LENGTH: 1261

; TYPE: DNA

; ORGANISM: Homo sapiens

; US-09-977-579-4

Alignment Scores:

Pred. No.: 3,53e-143 Length: 1261

Score: 1124.00 Matches: 215

Percent Similarity: 100.00% Conservatives: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 3 Gaps: 0

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Qy 1 MetProAlaPheAenArgLeuPheProLeuAlaSerLeuValLeuIleTyrTrpValSer 20
Db 376 ATGCGTGCCTTCAATAGATTGTTTCCCTCGCTGCTCTCTCGTGTCTATCTACTCGGTGTCAGT 435
Qy 21 ValCysPheProValCysValGluValProSerGluThrGluAlaValGlnGlyAsnPro 40
Db 436 GTCTGCTTCCCTGTGTGTGGAGTGCCTTCGAGAGCGGAGCGCGTGCAGGGCAACCC 495
Qy 41 MetLysLeuArgCysIleSerCysMetLysArgGluGlnValGluAlaThrValVal 60
Db 496 ATGAGCTGCTGCATCTCTGCTGATGAAGAGAGAGAGGTTGGAGGCCACACCGTGGTG 555
Qy 61 GluTrpPheTyrArgProGluGlyGlyAspPheLeuIleTyrGluTyrArgAsnGly 80
Db 556 GAATGGTTCTACAGCCCGAGCGGTAAAGATTTCCTTATTTACGAGTATCGGAATGGC 615
Qy 81 HisGlnGluValGluSerProPheGlnGlyArgGlnTrpAsnGlySerLysAspLeu 100
Db 616 CACAGGAGGTGGAGAGCCCTTTTCAGGGCGCTCGAGTGGAAATGGCAGCAAGACCTG 675
Qy 101 GlnAspValSerIleThrValLeuAsnValThrLeuAsnAspSerGlyLeuTyrThrCys 120
Db 676 CAGACGTGTCCATCACTGCTCACTCACTCTGAACGACTCTGGCCTCTACACCTGC 735
Qy 121 AsnValSerArgGluPheGluAlaHisArgProPheValLysThrThrArgLeu 140
Db 736 AATGTGTCCTCCGGAGTTTGTAGTTTGTAGCGCATCGGCCCTTTGTGAAGACGACGCGGTG 795
Qy 141 IleProLeuArgValThrGluGluAlaGlyGluAspPheThrSerValValSerGluIle 160
Db 796 ATCCCCCTTAAGAGTCACCTGAGGAGGCTGGAGAGACTTCACCTCTGTGGTCTCAGAAATC 855
Qy 161 MetMetTyrIleLeuLeuValPheLeuThrLeuTrpLeuIleGluMetIleTyrCys 180
Db 856 ATGATGTACATCTTCTGCTCTCTCCCTCCTCCTGCTGGCTGCTCATCGAGATGATATATGC 915
Qy 181 TyrArgLysValSerLysAlaGluGluAlaGlnGluAsnAlaSerAspTyrLeuAla 200
Db 916 TACAGAAAGGTCTCAAAAGCCGAAAGAGCGCAGCCCAAGAAACGCGTCTGTACTACCTTGCC 975

RESULT 2
US-10-482-834A-22
; Sequence 22, Application US/10482834A
; Publication No. US20050074764A1
; GENERAL INFORMATION:
; APPLICANT: Muller, John Charles
; APPLICANT: Harkin, Louise Anne
; APPLICANT: Dibbens, Michelle
; APPLICANT: Wallace, Robyn
; APPLICANT: Phillips, Hillary Anny
; APPLICANT: Heron, Sara Elizabeth
; APPLICANT: Berkovic, Samuel Frank
; APPLICANT: Scheffer, Ingrid Eileen
; APPLICANT: Bionomics Limited
; TITLE OF INVENTION: MUTATIONS IN ION CHANNELS
; FILE REFERENCE: 1386/17
; CURRENT APPLICATION NUMBER: US/10/482,834A
; CURRENT FILING DATE: 2004-01-02
; NUMBER OF SEQ ID NOS: 173
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 22
; LENGTH: 1261
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-482-834A-22
Alignment Scores:
US-09-977-579A-2 (1-215) x US-10-482-834A-22 (1-1261)
Qy 1 MetProAlaPheAenArgLeuPheProLeuAlaSerLeuValLeuIleTyrTrpValSer 20
Db 376 ATGCGTGCCTTCAATAGATTGTTTCCCTCGCTGCTCTCTCGTGTCTATCTACTCGGTGTCAGT 435
Qy 21 ValCysPheProValCysValGluValProSerGluThrGluAlaValGlnGlyAsnPro 40
Db 436 GTCTGCTTCCCTGTGTGTGGAGTGCCTTCGAGAGCGGAGCGCGTGCAGGGCAACCC 495
Qy 41 MetLysLeuArgCysIleSerCysMetLysArgGluGlnValGluAlaThrValVal 60
Db 496 ATGAGCTGCTGCATCTCTGCTGATGAAGAGAGAGGTTGGAGGCCACACCGTGGTG 555
Qy 61 GluTrpPheTyrArgProGluGlyGlyAspPheLeuIleTyrGluTyrArgAsnGly 80
Db 556 GAATGGTTCTACAGCCCGAGCGGTAAAGATTTCCTTATTTACGAGTATCGGAATGGC 615
Qy 81 HisGlnGluValGluSerProPheGlnGlyArgGlnTrpAsnGlySerLysAspLeu 100
Db 616 CACAGGAGGTGGAGAGCCCTTTTCAGGGCGCTCGAGTGGAAATGGCAGCAAGACCTG 675
Qy 101 GlnAspValSerIleThrValLeuAsnValThrLeuAsnAspSerGlyLeuTyrThrCys 120
Db 676 CAGACGTGTCCATCACTGCTCACTCACTCTGAACGACTCTGGCCTCTACACCTGC 735
Qy 121 AsnValSerArgGluPheGluAlaHisArgProPheValLysThrThrArgLeu 140
Db 736 AATGTGTCCTCCGGAGTTTGTAGTTTGTAGCGCATCGGCCCTTTGTGAAGACGACGCGGTG 795
Qy 141 IleProLeuArgValThrGluGluAlaGlyGluAspPheThrSerValValSerGluIle 160
Db 796 ATCCCCCTTAAGAGTCACCTGAGGAGGCTGGAGAGACTTCACCTCTGTGGTCTCAGAAATC 855
Qy 161 MetMetTyrIleLeuLeuValPheLeuThrLeuTrpLeuIleGluMetIleTyrCys 180
Db 856 ATGATGTACATCTTCTGCTCTCTCCCTCCTCCTGCTGGCTGCTCATCGAGATGATATATGC 915
Qy 181 TyrArgLysValSerLysAlaGluGluAlaGlnGluAsnAlaSerAspTyrLeuAla 200
Db 916 TACAGAAAGGTCTCAAAAGCCGAAAGAGCGCAGCCCAAGAAACGCGTCTGTACTACCTTGCC 975

RESULT 3
US-10-029-191-21
; Sequence 21, Application US/10029191
; Publication No. US20020160453A1
; GENERAL INFORMATION:
; APPLICANT: CURTIS, ROY A.J.
; TITLE OF INVENTION: NOVEL GENE ENCODING A SODIUM CHANNEL BETA-3 SUBUNIT
; TITLE OF INVENTION: PROTEIN
; FILE REFERENCE: 210147.00XX/5U1
; CURRENT APPLICATION NUMBER: US/10/029,191
; CURRENT FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 09/569,978
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/134,198
; PRIOR FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 645
; TYPE: DNA
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; ORGANISM: Rattus sp.
US-10-029-191-21

Alignment Scores:
Pred. No.: 5,09e-141 Length: 645
Score: 1105.00 Matches: 211
Percent Similarity: 98.14% Conservatives: 0
Best Local Similarity: 98.14% Mismatches: 4
Query Match: 98.31% Indels: 0
DB: 5 Gaps: 0

US-09-977-579A-2 (1-215) x US-10-029-191-21 (1-645)

Qy 1 MetProAlaPheAsnArgLeuPheProLeuAlaSerLeuValLeuIleTyrTrpValSer 20
Db 1 ATGCTGCTTCAACAGATTGCTTCCCTAGCTTCTCTAGTGCTCATCTACTGGGTGAGA 60

Qy 21 ValCysPheProValCysValGluValProSerGluThrGluAlaValGlnGlyAsnPro 40
Db 61 GTCTGCTTCCCTGCTGTGTGGAGTGCCTTCGGAGACAGAGCGGTGCAGGGCAATCCC 120

Qy 41 MetLysLeuArgCysIleSerCysMetLysArgGluGluValGluAlaThrThrValVal 60
Db 121 ATGAAGCTGAGGTGCATCTCTGTCATGAAGAGGAGGAGGTGCAGGCCCACTGTGGTG 180

Qy 61 GluTrpPheTyrArgProGluGlyGlyLysAspPheLeuIleTyrGluTyrArgAsnGly 80
Db 181 GAGTGGTTCACAGCCCTGAGGGCGGTAAAGATTTCCTTATATAGTATCGGAATGCG 240

Qy 81 HisGlnGluValGluSerProPheGlnGlyArgLeuGlnTrpAsnGlySerLysAspLeu 100
Db 241 CACAGGAGTGGAGAGCCCTTCAAGGCGCTGTCAGTGGAAATGGGAGCAAGACCTG 300

Qy 101 GlnAspValSerIleThrValLeuAsnValThrLeuAsnAspSerGlyLeuTyrThrCys 120
Db 301 CAGGAGGTATCCATCACTGTAATCAATGTCATTTGAATGATCTCTGGCTCTACATGC 360

Qy 121 AsnValSerArgGluPheGluPheGluAlaHisArgProPheValLysThrArgLeu 140
Db 361 AATGTGTCAGGAGGTTCGAAATTCAGGCGCACAGGCCCTTTTGTGAAGCACAGAGCTG 420

Qy 141 IleProLeuArgValThrGluGluAlaGlyGluAspPheThrSerValValSerGluIle 160
Db 421 ATACCTTTGCGAGTCACTGAAGAGCGGGAGAGACTTCACCTCGTGGTCTCGGAATC 480

Qy 161 MetMetTyrIleLeuLeuValPheLeuThrLeuIleThrLeuLeuIleGluMetIleTyrCys 180
Db 481 ATGATGTATACCTCTCTGCTTCTCTACCTTGTGGCTGTTTATTGAGATGATCTATTGC 540

Qy 181 TyrArgLysValSerLysAlaGluGluAlaGlnGluAsnAlaSerAspTyrLeuAla 200
Db 541 TACAGAAAGGTCTCTAAGGCCGGAAGAGGCGAGCACAGGAAATGCGCTGTGACTTGTCT 600

Qy 201 IleProSerGluAsnLysGluAsnSerAlaValProValGluGlu 215
Db 601 ATCCCTTCAGAGAACAGGAGAACTCTGTGGTACCTGTGGAGGAA 645

RESULT 4
US-09-977-579-3
; Sequence 3, Application US/09977579
; Publication No. US20040248240A1
; GENERAL INFORMATION:
; APPLICANT: Cambridge University Technical Services
; TITLE OF INVENTION: A novel family of beta sub-unit proteins from a voltage gated sod
; TITLE OF INVENTION: channel
; TITLE OF INVENTION: nucleic acids encoding them and therapeutic or diagnostic uses b
; FILE REFERENCE: 674558-2001
; CURRENT APPLICATION NUMBER: US/09/977,579
; PRIOR FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: PCT/EP00/01783
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60,129,473
; PRIOR FILING DATE: 2000-02-24

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; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 2220
; TYPE: DNA
; ORGANISM: rat
US-09-977-579-3

Alignment Scores:
Pred. No.: 3,45e-140 Length: 2220
Score: 1105.00 Matches: 211
Percent Similarity: 98.14% Conservatives: 0
Best Local Similarity: 98.14% Mismatches: 4
Query Match: 98.31% Indels: 0
DB: 3 Gaps: 0

US-09-977-579A-2 (1-215) x US-09-977-579-3 (1-2220)

Qy 1 MetProAlaPheAsnArgLeuPheProLeuAlaSerLeuValLeuIleTyrTrpValSer 20
Db 363 ATGCTGCTTCAACAGATTGCTTCCCTAGCTTCTCTAGTGCTCATCTACTGGGTGAGA 422

Qy 21 ValCysPheProValCysValGluValProSerGluThrGluAlaValGlnGlyAsnPro 40
Db 423 GTCTGCTTCCCTGCTGTGTGGAGTGCCTTCGGAGACAGAGCGGTGCAGGGCAATCCC 482

Qy 41 MetLysLeuArgCysIleSerCysMetLysArgGluGluValGluAlaThrThrValVal 60
Db 483 ATGAAGCTGAGGTGCATCTCTGTCATGAAGAGGAGGAGGTGGAGGCCCACTGTGGTG 542

Qy 61 GluTrpPheTyrArgProGluGlyGlyLysAspPheLeuIleTyrGluTyrArgAsnGly 80
Db 543 GAGTGGTTCACAGCCCTGAGGGCGGTAAAGATTTCCTTATATAGTATCGGAATGCG 602

Qy 81 HisGlnGluValGluSerProPheGlnGlyArgLeuGlnTrpAsnGlySerLysAspLeu 100
Db 603 CACAGGAGTGGAGAGCCCTTCAAGGCGCTGTCAGTGGAAATGGGAGCAAGACCTG 662

Qy 101 GlnAspValSerIleThrValLeuAsnValThrLeuAsnAspSerGlyLeuTyrThrCys 120
Db 663 CAGGAGGTATCCATCACTGTAATCAATGTCATTTGAATGATCTCTGGCTCTACATGC 722

Qy 121 AsnValSerArgGluPheGluPheGluAlaHisArgProPheValLysThrThrArgLeu 140
Db 723 AATGTGTCAGGAGGTTCGAAATTCAGGCGCACAGGCCCTTTTGTGAAGCACAGAGCTG 782

Qy 141 IleProLeuArgValThrGluGluAlaGlyGluAspPheThrSerValValSerGluIle 160
Db 783 ATACCTTTGCGAGTCACTGAAGAGCGGAGAACTTCACCTCGTGGTCTCGGAAATC 842

Qy 161 MetMetTyrIleLeuLeuValPheLeuThrLeuTrpLeuLeuIleGluMetIleTyrCys 180
Db 843 ATGATGTATACCTCTCTGCTTCTCTACCTTGTGGCTGTTTATTGAGATGATCTATTGC 902

Qy 181 TyrArgLysValSerLysAlaGluGluAlaGlnGluAsnAlaSerAspTyrLeuAla 200
Db 903 TACAGAAAGGTCTCTAAGGCCGGAAGAGGCGAGCACAGGAAATGCGCTGTGACTTGTCT 962

Qy 201 IleProSerGluAsnLysGluAsnSerAlaValProValGluGlu 215
Db 963 ATCCCTTCAGAGAACAGGAGAACTCTGTGGTACCTGTGGAGGAA 1007

RESULT 5
US-10-029-191-22
; Sequence 22, Application US/10029191
; Publication No. US20020160453A1
; GENERAL INFORMATION:
; APPLICANT: CURTIS, ROY A.J.
; TITLE OF INVENTION: NOVEL GENE ENCODING A SODIUM CHANNEL BETA-3 SUBUNIT
; TITLE OF INVENTION: PROTEIN
; FILE REFERENCE: 210147.00XX/5U1
; CURRENT APPLICATION NUMBER: US/10/029,191
; CURRENT FILING DATE: 2001-12-20

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; PRIOR APPLICATION NUMBER: 09/569,978
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/134,198
; PRIOR FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 2632
; TYPE: DNA
; ORGANISM: Rattus sp.
US-10-029-191-22

Alignment Scores:
Pred. No.: 4,49e-140 Length: 2632
Score: 1105.00 Matches: 211
Percent Similarity: 98.14% Conservativeness: 0
Best Local Similarity: 98.14% Mismatches: 4
Query Match: 98.31% Indels: 0
DB: 5 Gaps: 0

US-09-977-579A-2 (1-215) x US-10-029-191-22 (1-2632)

Qy 1 MetProAlaPheAsnArgLeuPheProLeuAlaSerLeuValLeuIleTyrTrpValSer 20
Db 78 ATGCCTGCCTTCACAGATTGCTTCCCTAGCTTCTCTAGTGCTCATCTACTGCGTCA 137
Qy 21 ValCysPheProValCysValGluValProSerGluThrGluAlaValGlnGlyAsnPro 40
Db 138 GTCTGCTTCCCTGTGTGTGGAAGTGCCTTCGGAGACAGAGCGGTGCGAGGCAATCCC 197
Qy 41 MetLysLeuArgCysIleSerCysMetLysArgGluGluValGluAlaThrValVal 60
Db 198 ATGAAGCTGAGGTGCATCTCTCGATGAAGAGGAGGAGGTGGAGGCCACCACCTGTGGTG 257
Qy 61 GluTrpPheTyrArgProGluGlyGlyLysAspPheLeuIleTyrGluTyrArgAsnGly 80
Db 258 GAGTGGTTCACAGCCCTGAGGCGGTAAAGATTTCCTTATATATAGTATCGGAATGGC 317
Qy 81 HisGlnGluValGluSerProPheGlnGlyArgLeuGlnTrpAsnGlySerLysAspLeu 100
Db 318 CACGAGGAAGTGGAGAGCCCTTCCAGGCCGTCTGCAGTGAATGGGAATGGAGCAAGACCTG 377
Qy 101 GlnAspValSerIleThrValLeuAsnValThrLeuAsnAspSerGlyLeuTyrThrCys 120
Db 378 CAGGACGTATCCATCACTGTAATCAATGTCAATTTGAATGACTCTGGCCTCTACACATGC 437
Qy 121 AsnValSerArgGluPheGluAlaHisArgProPheValLysThrArgLeu 140
Db 438 AATGTGTCAGGAGTTCGAATTCGAGGCACACAGGCCCTTTTGTGAAGACCACGAGACTG 497
Qy 141 IleProLeuArgValThrGluGluAlaGlyGluAspPheThrSerValValSerGluIle 160
Db 498 ATACCTTTGGCAGTCACTGAAGAGCGGAGAGACTTCACCTCCGTGGTCTCGGAATC 557
Qy 161 MetMetTyrIleLeuLeuValPheLeuThrLeuTrpLeuLeuIleGluMetIleTyrCys 180
Db 558 ATGATGTACATCCCTCGTCTTCTCTACCTTGTGGCTGTTTATTGAGATGATCTATTGC 617
Qy 181 TyrArgLysValSerLysAlaGluAlaAlaGlnGluAsnAlaSerAspTyrLeuAla 200
Db 618 TACAGAAAGTCTCTAAGGCCGAAGAGCGACAGGAAATGCGTCTGACTACCTTGCT 677

RESULT 6
US-10-029-191-1
; Sequence 1, Application US/10029191
; Publication No. US20020160453A1
; GENERAL INFORMATION:
; APPLICANT: CURTIS, ROY A.J.
; TITLE OF INVENTION: NOVEL GENE ENCODING A SODIUM CHANNEL BETA-3 SUBUNIT
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; TITLE OF INVENTION: PROTEIN
; FILE REFERENCE: 210147.00XX/SUI
; CURRENT APPLICATION NUMBER: US/10/029,191
; CURRENT FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 09/569,978
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/134,198
; PRIOR FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 3108
; TYPE: DNA
; ORGANISM: Rattus sp.
US-10-029-191-1

Alignment Scores:
Pred. No.: 5,81e-140 Length: 3108
Score: 1105.00 Matches: 211
Percent Similarity: 98.14% Conservativeness: 0
Best Local Similarity: 98.14% Mismatches: 4
Query Match: 98.31% Indels: 0
DB: 5 Gaps: 0

US-09-977-579A-2 (1-215) x US-10-029-191-1 (1-3108)

Qy 1 MetProAlaPheAsnArgLeuPheProLeuAlaSerLeuValLeuIleTyrTrpValSer 20
Db 78 ATGCCTGCCTTCACAGATTGCTTCCCTAGCTTCTCTAGTGCTCATCTACTGCGTCA 137
Qy 21 ValCysPheProValCysValGluValProSerGluThrGluAlaValGlnGlyAsnPro 40
Db 138 GTCTGCTTCCCTGTGTGTGGAAGTGCCTTCGGAGACAGAGCGGTGCGAGGCAATCCC 197
Qy 41 MetLysLeuArgCysIleSerCysMetLysArgGluGluValGluAlaThrValVal 60
Db 198 ATGAAGCTGAGGTGCATCTCTCGATGAAGAGGAGGAGGTGGAGGCCACCACCTGTGGTG 257
Qy 61 GluTrpPheTyrArgProGluGlyGlyLysAspPheLeuIleTyrGluTyrArgAsnGly 80
Db 258 GAGTGGTTCACAGCCCTGAGGCGGTAAAGATTTCCTTATATATAGTATCGGAATGGC 317
Qy 81 HisGlnGluValGluSerProPheGlnGlyArgLeuGlnTrpAsnGlySerLysAspLeu 100
Db 318 CACGAGGAAGTGGAGAGCCCTTCCAGGCCGTCTGCAGTGAATGGGAATGGAGCAAGACCTG 377
Qy 101 GlnAspValSerIleThrValLeuAsnValThrLeuAsnAspSerGlyLeuTyrThrCys 120
Db 378 CAGGACGTATCCATCACTGTAATCAATGTCAATTTGAATGACTCTGGCCTCTACACATGC 437
Qy 121 AsnValSerArgGluPheGluAlaHisArgProPheValLysThrArgLeu 140
Db 438 AATGTGTCAGGAGTTCGAATTCGAGGCACACAGGCCCTTTTGTGAAGACCACGAGACTG 497
Qy 141 IleProLeuArgValThrGluGluAlaGlyGluAspPheThrSerValValSerGluIle 160
Db 498 ATACCTTTGGCAGTCACTGAAGAGCGGAGAGACTTCACCTCCGTGGTCTCGGAATC 557
Qy 161 MetMetTyrIleLeuLeuValPheLeuThrLeuTrpLeuLeuIleGluMetIleTyrCys 180
Db 558 ATGATGTACATCCCTCGTCTTCTCTACCTTGTGGCTGTTTATTGAGATGATCTATTGC 617
Qy 181 TyrArgLysValSerLysAlaGluAlaAlaGlnGluAsnAlaSerAspTyrLeuAla 200
Db 618 TACAGAAAGTCTCTAAGGCCGAAGAGCGACAGGAAATGCGTCTGACTACCTTGCT 677

RESULT 7
US-10-450-763-22568
; Sequence 22568, Application US/10450763
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Publication No. US20050196754A1
GENERAL INFORMATION:
APPLICANT: Hyseq, Inc
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
FILE REFERENCE: 790CIP3/US
CURRENT APPLICATION NUMBER: US/10/450,763
CURRENT FILING DATE: 2003-06-11
PRIORITY APPLICATION NUMBER: PCT/US01/08631
PRIOR FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: 09/540,217
PRIOR FILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: 09/649,167
PRIOR FILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 60736
SOFTWARE: Custom
SEQ ID NO 22568
LENGTH: 1195
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SIMILAR
LOCATION: (518)..(1051)
OTHER INFORMATION: 91% homologous to Homo sapiens voltage-gated sodium channel
OTHER INFORMATION: beta-3 subunit, accession number AJ243396, Smith-Waterman Score=826
US-10-450-763-22568
Alignment Scores:
Pred. No.: 3,17e-116 Length: 1195
Score: 927.50 Matches: 184
Percent Similarity: 94.42% Conservative: 2
Best Local Similarity: 93.40% Mismatches: 9
Query Match: 82.52% Indels: 2
DB: Gaps: 1
US-09-977-579A-2 (1-215) x US-10-450-763-22568 (1-1195)
QY 1 MetProAlaPheAsnArgLeuPheProLeuAlaSerLeuValLeuIleTyrTrpValSer 20
DB 463 ATGCCTGCTTCAATAGATTGTTCCCTGGCTTCTCTCGTGTATCTACTGAGTCAGT 522
QY 21 ValCysPheProValCysValGlu-ValProSerGluThrGluAla---ValGlnGlyAs 39
DB 523 GTCTGCTTCCCTGTGTGGGGGAAAGTGCCCTTAGAAAACGGGGGGCGGACGGCTAA 582
QY 39 nProMetLysLeuArgCysIleSerCysMetLysArgGluGluValGluAlaThrVa 59
DB 583 CCCCATGAAGCTGCGCTGCATCTCTGCATGAAGAGAGAGAGGTGGAGGCCACCACGGT 642
QY 59 lValGluTrpPheTyrArgProGluGlyGlyLysAspPheLeuIleTyrGluTyrArg 79
DB 643 GGTGGAATGGTTCTACAGCCCGAGGGCGGTAAAGATTTCCTTATTACGAGTATCGGAA 702
QY 79 nGlyHisGlnGluValGluSerProPheGlnGlyArgLeuGlnTrpAsnGlySerLys 99
DB 703 TGCCACACAGAGAGGTGGAGAGCCCTTTTCAGGGGGCCCTGCAGTGGATGGCAGCAGA 762
QY 99 pLeuGlnAspValSerIleThrValLeuAsnValThrLeuAsnAspSerGlyLeuTyrTh 119
DB 763 CTGCAGGAGGTGTCATCCTACCTGCTCAACGCTCACTCTGAACGACTCTGGCCTCTAC 822
QY 119 rCysAsnValSerArgGluPheGluPheGluAlaHisArgPropheValLysThrAr 139
DB 823 CTGCAATGTGTCGCGGAGTTTGAGTTTGAGGCGCATCGGCCCTTTGTGAAGACACCGG 882
QY 139 gLeuIleProLeuArgValThrGluGluAlaGlyGluAspPheThrSerValValSerG 159
DB 883 GCTGATCCCCCTTAAAGATCACCAGAGAGGCTGGAGGAGCTTCACCTCTGTGCTCTCAG 942
QY 159 uIleMetMetTyrIleLeuLeuValPheLeuThrIleuTrpLeuLeuIleGluMetIleTy 179
DB 943 AATCATGATGATACCTTCTGCTCTCTCCTACCTTGTGGCTGCTCATCGAGATGATATA 1002
QY 179 rCysTyrArgLysValSerLysAlaGluGluAlaGlnGluAsnAla 195

Db 1003 TTGCTACAGACAGGTCTCAAAAGCCGAAGGAGCGACCCCAAGAAACGCG 1051
RESULT 8
US-10-450-763-22567
Sequence 22567, Application US/10450763
Publication No. US20050196754A1
GENERAL INFORMATION:
APPLICANT: Hyseq, Inc
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
FILE REFERENCE: 790CIP3/US
CURRENT APPLICATION NUMBER: US/10/450,763
CURRENT FILING DATE: 2003-06-11
PRIORITY APPLICATION NUMBER: PCT/US01/08631
PRIOR FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: 09/540,217
PRIOR FILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: 09/649,167
PRIOR FILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 60736
SOFTWARE: Custom
SEQ ID NO 22567
LENGTH: 3531
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SIMILAR
LOCATION: (300)..(407)
OTHER INFORMATION: 94% homologous to Homo sapiens putative kruppel-related zinc
OTHER INFORMATION: finger protein NY-REN-23 antigen, accession number AF155101, Smith-
OTHER INFORMATION: Waterman Score=180.
US-10-450-763-22567
Alignment Scores:
Pred. No.: 2e-83 Length: 3531
Score: 694.00 Matches: 130
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 61.74% Indels: 0
DB: Gaps: 0
US-09-977-579A-2 (1-215) x US-10-450-763-22567 (1-3531)
QY 19 ValSerValCysPheProValCysValGluValProSerGluThrGluAlaValGlnGly 38
DB 2959 GTGAGTGTCTCCCTGCTGTGTGGAAGTGCCTCGAGACGGAGCGCGTGCAGGCG 3018
QY 39 AsnProMetLysLeuArgCysIleSerCysMetLysArgGluGluValGluAlaThrThr 58
DB 3019 AACCCCATGAAGCTGCGCTGCATCTCTGCATGAAGAGAGAGAGGTGGAGGCCACCAG 3078
QY 59 ValValGluTrpPheTyrArgProGluGlyGlyLysAspPheLeuIleTyrGluTyrArg 78
DB 3079 GTGGTGGAAATGGTTCTACAGGCCCGGCGGTAAAGATTTCCTTATTACGAGTATCG 3138
QY 79 AsnGlyHisGlnGluValGluSerProPheGlnGlyArgLeuGlnTrpAsnGlySerLys 98
DB 3139 AATGCCACACAGAGGTGGAGAGCCCTTTTCAGGGGGCCCTGCAGTGGATGGCAGCAAG 3198
QY 99 AspLeuGlnAspValSerIleThrValLeuAsnValThrLeuAsnAspSerGlyLeuTyr 118
DB 3199 GACCTGCAGGAGGTGTCATCCTCAACGCTCACTCTGAACGACTCTGGCCCTCTAC 3258
QY 119 ThrCysAsnValSerArgGluPheGluAlaHisArgPropheValLysThrThr 138
DB 3259 ACCTGCAATGTGTCCCGGAGTTTGAGTTTGAGGCGCATCGGCCCTTTGTGAAGACGAG 3318
QY 139 ArgLeuIleProLeuArgValThrGluGlu 148
DB 3319 CGGCTGATCCCTTAAGAGTCAACGAGGAG 3348
RESULT 9
US-11-060-756-2816

US-10-723-860-2247
; Sequence 2247, Application US/10723860
; Publication No. US2004025360A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Nataasha
; APPLICANT: Gineburg, Wendy M.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &
; TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
; FILE REFERENCE: 03882.0193.NPUS01
; CURRENT APPLICATION NUMBER: US/10/723,860
; PRIOR FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 60/429,739
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 8393
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2247
; LENGTH: 1335
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-860-2247

Alignment Scores:
Pred. No.: 1.01e-53 Length: 1335
Score: 473.00 Matches: 109
Percent Similarity: 63.35% Conservative: 31
Best Local Similarity: 49.32% Mismatches: 71
Query Match: 42.08% Indels: 10
DB: 8 Gaps: 6

US-09-977-579A-2 (1-215) x US-10-723-860-2247 (1-1335)

Qy 3 AlaPheAsnArgLeuPheProLeuAlaSerLeuValLeuIleTyrTrpValSerValCys 22
Db 22 GCCATTGGGGAGGCTG-----CTGGCTTAGTGTGGCGCGGCACTGGTCTCAGCC 75
Qy 23 PheProValCysValGluValProSerGluThrGluAlaValGlnGlyAsnProMetLys 42
Db 76 TCGGGGGCTCGGTGGAGGTGGACTCGAGACCGAGCGCGGTGTATGGATGACCTTCAAA 135
Qy 43 LeuArgCysIleSerCysMetLysArgGluValGluAlaThrValGluTrp 62
Db 136 ATCTTTTGATCTCTCTCAAGCGCGGAGGAGTTGTCAAGATCTCGCGCTATGAGATGG 195
Qy 63 PheTyrArgProGluGlyGlyLysAspPheLeu---IleTyrGluTyrArgAsnGlyHis 81
Db 196 ACCTTCGCCCAAGAGGCACTGAGGAGTTTGTCAAGATCTCGCGCTATGAGATGG 255
Qy 82 GlnGluValGluSerPro-----PheGlnGlyArgLeuGlnTrpAsnGlySer----- 97
Db 256 TTGCAGCTGGAGGAGGATGAGCGCTTCAGGGCGCGGTGGTGGATGGAGCGCGGGC 315
Qy 98 ---LysAspLeuGlnAspValSerIleThrValLeuAsnValThrLeuAsnAspSerGly 116
Db 316 ACCAAGACCTGCAGGATCTCTATCTCATCACCAATGTCTACCTACACCACTCGGGC 375
Qy 117 LeuTyrThrCysAsnValSerArgGluPheGluAlaHisArgProPheValLys 136
Db 376 GACTACGAGTGCCACGCTCTACCGCTCTCTTCGAAATACAGACCAACACCGAGC 435
Qy 137 ThrThrArgLeuIleProLeuArgValThrGluGluAlaGlyGluAspPheThrSerVal 156
Db 436 GTCGTCAAGAAATCCCATTTAGGTAGTGGACCAAGCCCAACAGAGACATGGCATCCATC 495
Qy 157 ValSerGluIleMetMetTyrIleLeuLeuValPheLeuThrLeuTrpLeuLeuGlu 176
Db 496 GTGCTCAGATCATGATGATGTCTCATTTGGTGTGGTGGTGGTGGTGGTGGTGGTGG 555
Qy 177 MetIleTyrCysTyrArgLysValSerLysAla---GluGluAlaAlaGlnGluAsnAla 195
Db 556 ATGATTTACTCTCAAGAAGATCGCTCGCCCGGAGAGTGTGTGACCATATGGCTCGTGG 615
Qy 196 SerAspTyrLeuAlaIleProSerGluAsnLysGluAsn---SerAlaValProValGlu 214

Db 616 TCGGAATACCTGGCCATCACCTCTGAAAGCAAGAGAACTGCACGGCGTCCAGGTGGCC 675
Qy 215 Glu 215
Db 676 GAA 678

RESULT 15
US-10-477-272-1
; Sequence 1, Application US/10477272
; Publication No. US20040191791A1
; GENERAL INFORMATION:
; APPLICANT: Bionomics Limited
; TITLE OF INVENTION: P12
; FILE REFERENCE: SCNIB (R85C)
; CURRENT APPLICATION NUMBER: US/10/477,272
; CURRENT FILING DATE: 2003-11-10
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1414
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-477-272-1

Alignment Scores:
Pred. No.: 1.1e-53 Length: 1414
Score: 473.00 Matches: 109
Percent Similarity: 63.35% Conservative: 31
Best Local Similarity: 49.32% Mismatches: 71
Query Match: 42.08% Indels: 10
DB: 8 Gaps: 6

US-09-977-579A-2 (1-215) x US-10-477-272-1 (1-1414)

Qy 3 AlaPheAsnArgLeuPheProLeuAlaSerLeuValLeuIleTyrTrpValSerValCys 22
Db 98 GCCATTGGGGAGGCTG-----CTGGCTTAGTGTGGCGCGGCACTGGTCTCAGCC 151
Qy 23 PheProValCysValGluValProSerGluThrGluAlaValGlnGlyAsnProMetLys 42
Db 152 TCGGGGGCTCGGTGGAGGTGGACTCGAGACCGAGCGCGGTGTATGGGATGACCTTCAAA 211
Qy 43 LeuArgCysIleSerCysMetLysArgGluValGluAlaThrValGluTrp 62
Db 212 ATCTTTTGATCTCTCTCAAGCGCGGAGGAGTTTGTCAAGATCTCGCGCTATGAGATGG 271
Qy 63 PheTyrArgProGluGlyGlyLysAspPheLeu---IleTyrGluTyrArgAsnGlyHis 81
Db 272 ACCTTCGCCCAAGGCACTGAGGAGTTTGTCAAGATCTCGCGCTATGAGATGG 331
Qy 82 GlnGluValGluSerPro-----PheGlnGlyArgLeuGlnTrpAsnGlySer----- 97
Db 332 TTGCAGCTGGAGGAGGATGAGTGTTCGAGGGCGCGGTGGTGGATGGAGCGCGGGC 391
Qy 98 ---LysAspLeuGlnAspValSerIleThrValLeuAsnValThrLeuAsnAspSerGly 116
Db 392 ACCAAGACCTGCAGGATCTCTATCTCATCACCAATGTCTACCTACACCACTCGGGC 451
Qy 117 LeuTyrThrCysAsnValSerArgGluPheGluAlaHisArgProPheValLys 136
Db 452 GACTACGAGTGCCACGCTCTACCGCTCTCTTCGAAATACAGACCAACACCGAGC 511
Qy 137 ThrThrArgLeuIleProLeuArgValThrGluGluAlaGlyGluAspPheThrSerVal 156
Db 512 GTCGTCAAGAAATCCCATTTAGGTAGTGGACCAAGCCCAACAGAGACATGGCATCCATC 571
Qy 157 ValSerGluIleMetMetTyrIleLeuLeuValPheLeuThrLeuTrpLeuLeuGlu 176
Db 572 GTGCTCAGATCATGATGATGTCTCATTTGGTGTGGTGGTGGTGGTGGTGGTGGTGG 631
Qy 177 MetIleTyrCysTyrArgLysValSerLysAla---GluGluAlaAlaGlnGluAsnAla 195

Db	632	ATGATTCTCTACAAAGATCGCTGCCGCCACGGAGACTGTGTCACAGGAGATGCC	691
Qy	196	SerAspTyrLeuAlaIleProSerGluAsnLysGluAsn---SerAlaValProValGlu	214
Db	692	TCGGATACCTGGCCATCACCTCTGAAAGCAAGAGAACTGCACGGCGGTCCAGGTGCC	751
Qy	215	Glu	215
Db	752	GAA	754

Search completed: January 5, 2006, 19:11:07
Job time : 788 secs

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: January 5, 2006, 16:44:17 ; Search time 203 Seconds
(without alignments)
772.027 Million cell updates/sec

Title: US-09-977-579A-2
Perfect score: 1124
Sequence: 1 MPARNRPLPLASLVLIYVWS.....SDYLAIPSENKENSAPVVEE 215

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Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4637609 seqs, 364468668 residues

Total number of hits satisfying chosen parameters: 9275218

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
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-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA New.*

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3:	/cgn2_6/ptodata/1/pubnpa/US07 NEW PUB.seq.*	
4:	/cgn2_6/ptodata/1/pubnpa/PCT NEW PUB.seq.*	
5:	/cgn2_6/ptodata/1/pubnpa/US03 NEW PUB.seq.*	
6:	/cgn2_6/ptodata/1/pubnpa/US10 NEW PUB.seq.*	
7:	/cgn2_6/ptodata/1/pubnpa/US11 NEW PUB.seq.*	
8:	/cgn2_6/ptodata/1/pubnpa/US11 NEW PUB.seq2.*	
9:	/cgn2_6/ptodata/1/pubnpa/US11 NEW PUB.seq3.*	
10:	/cgn2_6/ptodata/1/pubnpa/US60 NEW PUB.seq.*	

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1124	100.0	1261	US-10-374-954-8	Sequence 8, Appli
2	1105	98.3	3820	US-11-136-527-750	Sequence 750, App
3	473	42.1	1335	US-10-374-954-4	Sequence 4, Appli
4	472	42.0	1400	US-11-136-527-6498	Sequence 6498, Ap
5	472	42.0	1490	US-10-533-355-7	Sequence 7, Appli
6	472	42.0	1508	US-11-136-527-2402	Sequence 2402, Ap
7	241	21.4	880	US-10-750-185-44336	Sequence 44336, A
8	241	21.4	880	US-10-750-623-44336	Sequence 44336, A

9	165.5	14.7	150468	7	US-11-112-908-56	Sequence 56, Appl
10	165.5	14.7	193789	7	US-11-112-908-55	Sequence 55, Appl
11	147	13.1	673	7	US-11-080-991-111	Sequence 111, Appl
12	147	13.1	1371	6	US-10-131-826A-487	Sequence 487, App
13	131	11.7	1777	6	US-10-131-826A-529	Sequence 529, App
14	114	10.1	1015	6	US-11-136-527-2158	Sequence 2158, Ap
15	110.5	9.8	648	6	US-10-374-954-6	Sequence 6, Appli
16	109	9.7	1630	6	US-10-131-826A-519	Sequence 519, App
17	108.5	9.7	2458	6	US-10-131-826A-387	Sequence 387, App
18	105	9.3	1497	6	US-10-750-185-44339	Sequence 44339, A
19	105	9.3	1497	6	US-10-750-623-44339	Sequence 44339, A
20	102.5	9.1	138821	7	US-11-121-086-80	Sequence 80, Appl
21	100	8.9	600	7	US-11-136-527-6254	Sequence 6254, Ap
22	99.5	8.9	1324	6	US-10-750-185-44343	Sequence 44343, A
23	99.5	8.9	1324	6	US-10-750-623-44343	Sequence 44343, A
24	98.5	8.8	396	6	US-10-959-310-22	Sequence 22, Appl
25	98.5	8.8	433	7	US-11-012-353-62	Sequence 62, Appl
26	98.5	8.8	433	7	US-11-012-353-66	Sequence 66, Appl
27	96.5	8.6	2749	6	US-10-131-826A-385	Sequence 385, App
28	95.5	8.5	2311	7	US-11-136-527-3513	Sequence 3513, Ap
29	94.5	8.4	2793	6	US-10-775-169-228	Sequence 228, App
30	93.5	8.3	396	6	US-10-932-334-49	Sequence 49, Appl
31	93.5	8.3	1506	6	US-10-750-185-30397	Sequence 30397, A
32	93.5	8.3	1506	6	US-10-750-623-30397	Sequence 30397, A
33	93	8.3	2906	6	US-10-131-826A-367	Sequence 367, App
34	92.5	8.2	393	6	US-10-789-273-13	Sequence 13, Appl
35	92.5	8.2	393	7	US-11-125-837-31	Sequence 31, Appl
36	92	8.2	1116	7	US-11-087-177-38	Sequence 38, Appl
37	90	8.0	1326	6	US-10-055-877-76	Sequence 76, Appl
38	90	8.0	1650	7	US-11-000-688-144	Sequence 144, App
39	90	8.0	2473	7	US-11-080-991-77	Sequence 77, Appl
40	90	8.0	2537	7	US-11-102-978-8	Sequence 8, Appli
41	90	8.0	162085	7	US-11-121-086-7	Sequence 7, Appli
42	89.5	8.0	438	7	US-11-012-353-48	Sequence 48, Appl
43	89	7.9	1077	7	US-11-136-527-613	Sequence 613, App
44	89	7.9	3286	7	US-11-136-527-158	Sequence 158, App
45	89	7.9	54946	6	US-10-995-561-13479	Sequence 13479, A

ALIGNMENTS

RESULT 1
US-10-374-954-8
; Sequence 8, Application US/10374954
; Publication No. US20050260576A1
; GENERAL INFORMATION:
; APPLICANT: Vanderbilt University
; APPLICANT: George, Alfred L
; APPLICANT: Lossin, Christoph
; TITLE OF INVENTION: HETEROLOGOUS EXPRESSION SYSTEM FOR STUDYING RECOMBINANT HUMAN
; TITLE OF INVENTION: BRAIN VOLTAGE-GATED SODIUM CHANNEL, SCN1A
; FILE REFERENCE: 1242/41/2
; CURRENT APPLICATION NUMBER: US/10/374,954
; CURRENT FILING DATE: 2003-02-25
; PRIOR APPLICATION NUMBER: US 60/359,382
; PRIOR FILING DATE: 2002-02-25
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
; LENGTH: 1261
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (376)..(1023)
US-10-374-954-8
Alignment Scores:
Pred. No.: 8.27e-139
Score: 1124.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Length: 1261
Matches: 215
Conservative: 0
Indels: 0

DB: 6 Gaps: 0

US-09-977-579A-2 (1-215) x US-10-374-954-8 (1-1261)

Qy 1 MetProAlaPheAsnArgLeuPheProLeuAlaSerLeuValLeuIleTyrTrpValSer 20
 376 ATGCTGCTTCAATAGATTGTTCCCTGGCTTCTCTCGTCTATCTACTTGGTCACT 435

Qy 21 ValCysPheProValCysValGluValProSerGluThrGluAlaValGlnGlyAsnPro 40
 436 GTCTGCTTCCCTGTGTGTGGAAGTCCCTCGAGACGGAGCGGTGCAGGGCAACCCC 495

Qy 41 MetLysLeuArgCysIleSerCysMetLysArgGluValGluAlaThrValVal 60
 496 ATGAAGTGGCTGCATCTCTCTCATGAAGAGAGAGGAGGTGGAGGCCACACCGTGGTG 555

Qy 61 GluTrpPheTyrArgProGluGlyGlyLysAspPheLeuIleTyrGluTyrArgAsnGly 80
 556 GAATGGTCTACAGCCCGAGGGCGGTAAAGATTTCCTTATTACGAGTATCGGAATGGC 615

Qy 81 HisGlnGluValGluSerProPheGlnGlyArgLeuGlnTrpAsnGlySerLysAspLeu 100
 616 CACCAGAGGTGGAGAGCCCTTTTCAGGGCGCTCGAGTGAATGGCAGCAGGACCTG 675

Qy 101 GlnAspValSerIleThrValLeuAsnValThrLeuAsnAspSerGlyLeuTyrThrCys 120
 676 CAGACGTGTCCATCACTGTCTCAACGTCACTCTGAACGACTCTGGCCCTCTACACCTGC 735

Qy 121 AsnValSerArgGluPheGluAlaHisArgProPheValLysThrThrArgLeu 140
 736 AATGTGTCCCGGAGTTGAGTTGAGCGCATCGGCCCTTTGTGAAGACGACGCGCTG 795

Qy 141 IleProLeuArgValThrGluGluAlaGlyGluAspPheThrSerValSerGluIle 160
 796 ATCCCTTAAAGTCAACGAGAGGCTGGAGAGACTTCACTCTGTGTGTCTCAGAAATC 855

Qy 161 MetMetTyrIleLeuLeuValPheLeuThrLeuTrpLeuIleGluMetIleTyrCys 180
 856 ATGATGTACATCTCTGTGTCTTCTCACCCTGTGGCTGTCTCATCGAGATGATATATGC 915

Qy 181 TyrArgLysValSerLysAlaGluGluAlaGlnGluAsnAlaSerAspTyrLeuAla 200
 916 TACAGAAAGTCTCAAAAGCCGAGAGCGCCCAAGAAACCGTCTGACTACCTTTGCC 975

Qy 201 IleProSerGluAsnLysGluAsnSerAlaValProValGluGlu 215
 976 ATCCCATCTGAGAACAAAGGAGAACTCTCGGTACCAGTGGAGGAA 1020

RESULT 2

US-11-136-527-750

; Sequence 750, Application US/11136527

; Publication No. US20050287570A1

; GENERAL INFORMATION:

; APPLICANT: Wyeth

; APPLICANT: Mounts, William M

; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes

; FILE REFERENCE: 031896-041000 (AM101086)

; CURRENT APPLICATION NUMBER: US/11/136,527

; CURRENT FILING DATE: 2005-05-25

; PRIOR APPLICATION NUMBER: US 60/574,294

; PRIOR FILING DATE: 2005-05-26

; NUMBER OF SEQ ID NOS: 362830

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 750

; LENGTH: 3820

; TYPE: DNA

; ORGANISM: Rattus norvegicus

US-11-136-527-750

Alignment Scores:

Pred. No.: 1.54e-135 Length: 3820

Score: 1105.00 Matches: 211

Percent Similarity: 98.14% Conservative: 0

Best Local Similarity: 98.14% Mismatches: 4

Query Match: 98.31% Indels: 0

DB: 7 Gaps: 0

US-09-977-579A-2 (1-215) x US-11-136-527-750 (1-3820)

Qy 1 MetProAlaPheAsnArgLeuPheProLeuAlaSerLeuValLeuIleTyrTrpValSer 20
 363 ATGCTGCTTCAACAGATTGCTTCCCTAGCTTCTCTAGTCTCATCTACTTGGTCACT 422

Qy 21 ValCysPheProValCysValGluValProSerGluThrGluAlaValGlnGlyAsnPro 40
 423 GTCTGCTTCCCTGTGTGTGGAAGTCCCTCGAGACAGAAAGCGGTGCAGGGCAATCCC 482

Qy 41 MetLysLeuArgCysIleSerCysMetLysArgGluValGluAlaThrValVal 60
 483 ATGAAGTGGAGTGCATCTCTCTCATGAAGAGGAGGAGGTGGAGGCCACACCTGTGGTG 542

Qy 61 GluTrpPheTyrArgProGluGlyGlyLysAspPheLeuIleTyrGluTyrArgAsnGly 80
 543 GATGTGTCTACAGGCTTGAAGCGGTAAAGATTTCCTTATATATATGAGTATCGGAATGGC 602

Qy 81 HisGlnGluValGluSerProPheGlnGlyArgLeuGlnTrpAsnGlySerLysAspLeu 100
 603 CACCAGAGGTGGAGAGCCCTTTCCAAAGGCGCTCTGCAGTGAATGGGAGCAAGACCTG 662

Qy 101 GlnAspValSerIleThrValLeuAsnValThrLeuAsnAspSerGlyLeuTyrThrCys 120
 663 CAGGACGTATCCATCACTGTCTCAATGTCACTTTGAATGACTCTGGCCCTCTACACATGC 722

Qy 121 AsnValSerArgGluPheGluAlaHisArgProPheValLysThrThrArgLeu 140
 723 AATGTGTCCAGGAGTTTGAATTCGAGGCGACACAGGCCCTTTGTGAAGACACGAGACTG 782

Qy 141 IleProLeuArgValThrGluGluAlaGlyGluAspPheThrSerValSerGluIle 160
 783 ATACCTTTGGAGTCACTGAAGAGGCGGAGAGACTTCACTCCGTGGTCTCGAAATC 842

Qy 161 MetMetTyrIleLeuLeuValPheLeuThrLeuTrpLeuIleGluMetIleTyrCys 180
 843 ATGATGTACATCTCTCTGTGTCTTCTCACCCTGTGGCTGTATTATGAGATGATCTATTGC 902

Qy 181 TyrArgLysValSerLysAlaGluGluAlaGlnGluAsnAlaSerAspTyrLeuAla 200
 903 TACAGAAAGTCTCTAAGCGCCGAGAGGCGACAGCAAGAAATGGCTCTGACTACCTTGTCT 962

Qy 201 IleProSerGluAsnLysGluAsnSerAlaValProValGluGlu 215
 963 ATCCCTTCAGAAACAAGGAGAACTCTGTGTGTACCTGTGGAGGAA 1007

RESULT 3

US-10-374-954-4

; Sequence 4, Application US/10374954

; Publication No. US20050260576A1

; GENERAL INFORMATION:

; APPLICANT: Vanderbilt University

; APPLICANT: George, Alfred L

; APPLICANT: Lossin, Christoph

; TITLE OF INVENTION: HETEROLOGOUS EXPRESSION SYSTEM FOR STUDYING RECOMBINANT HUMAN

; TITLE OF INVENTION: BRAIN VOLTAGE-GATED SODIUM CHANNEL, SCN1A

; FILE REFERENCE: 1242/41/2

; CURRENT APPLICATION NUMBER: US/10/374,954

; CURRENT FILING DATE: 2003-02-25

; PRIOR APPLICATION NUMBER: US 60/359,382

; PRIOR FILING DATE: 2002-02-25

; NUMBER OF SEQ ID NOS: 27

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 4

; LENGTH: 1335

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

```

; LOCATION: (25)..(681)
; US-10-374-954-4

Alignment Scores:
Pred. No.: 3.89e-52 Length: 1335
Score: 473.00 Matches: 109
Percent Similarity: 63.35% Conservative: 31
Best Local Similarity: 49.32% Mismatches: 71
Query Match: 42.08% Indels: 10
DB: 6 Gaps: 6

US-09-977-579A-2 (1-215) x US-10-374-954-4 (1-1335)

Qy 3 AlaPheAnArgLeuPheProLeuAlaSerLeuValLeuLeuTyrTrpValSerValCys 22
Db 22 GCCATGGGGAGGCTG-----CTGGCTTATGTTGGCGCGGCACCTGCTCTCTCAGCC 75

Qy 23 PheProValCysValGluValProSerGluThrGluAlaValGlnGlyAsnProMetLys 42
Db 76 TCGGGGGCTCGTGGAGTGGACTCGGAGACCGGCGCGTGTATGGATGACCTTCAAA 135

Qy 43 LeuArgCysIleSerCysMetLysArgGluGluValGluAlaThrThrValValGluTrp 62
Db 136 ATTCTTTCATCTCTCTCAAGCGCGCAGCGAGACCAACGCTGAGACCTTCCACGAGTG 195

Qy 63 PheTyrArgProGluGlyCysLysAspPheLeu---IleTyrGluTyrArgAsnGlyHis 81
Db 196 ACCTTCCGCCAGAGGGCAGTGGAGGATTTGTCAAGATCTCTCGCTATGAGAAATGAGGTG 255

Qy 82 GlnGluValGluSerPro-----PheGlnGlyArgLeuGlnTrpAsnGlySer----- 97
Db 256 TTGCAGCTGGAGGAGGATGAGCGCTTCAGGGCGCGTGTGGATGGGCGCGGGC 315

Qy 98 ---LysAspLeuGlnAspValSerIleThrValLeuAsnValThrLeuAsnAspSerGly 116
Db 316 ACCAAGACCTGCAGATCTGTCTATCTTCATCACCATTGTCACTCAACACCTCGGGC 375

Qy 117 LeuTyrThrCysAsnValSerArgGluPheGluAlaHisArgProPheValLys 136
Db 376 GACTACGAGTGCACGCTACCGCTCTCTTTCGAAACTACGACGACCAACACCGC 435

Qy 137 ThrThrArgLeuIleProLeuArgValThrGluGluAlaGlyGluAspPheThrSerVal 156
Db 436 GTCGTCAGAGATCCCATTTGAGGTAGTGGCAAGCCACAGACATGTCATCCATC 495

Qy 157 ValSerGluIleMetMetTyrIleLeuLeuValPheLeuThrLeuTrpLeuLeuGlu 176
Db 496 GTGCTGAGATCATGTATGTCTCATTTGGTGTGGACCATATGGCTCGTGCAGAG 555

Qy 177 MetIleTyrCysTyrArgLysValSerLysAla---GluGluAlaGlnGluAsnAla 195
Db 556 ATGATTTACTGTACAAGAAGATCGTCCGCCACGAGACTGCTGCGACAGAGAAATGCC 615

Qy 196 SerAspTyrLeuAlaIleProSerGluAsnLysGluAsn---SerAlaValProValGlu 214
Db 616 TCGGAATACCTGCCATCACCTCTGAAACCAAGAGAACTGCACGGGCTCCAGGTGCC 675

Qy 215 Glu 215
Db 676 GAA 678

RESULT 4
US-11-136-527-6498
; Sequence 6498, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294

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; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6498
; LENGTH: 1400
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-6498

Alignment Scores:
Pred. No.: 5.69e-52 Length: 1400
Score: 472.00 Matches: 105
Percent Similarity: 64.49% Conservative: 33
Best Local Similarity: 49.07% Mismatches: 68
Query Match: 41.99% Indels: 8
DB: 7 Gaps: 5

US-09-977-579A-2 (1-215) x US-11-136-527-6498 (1-1400)

Qy 10 LeuAlaSerLeuValLeuIleTyrTrpValSerValCysPheProValCysValGluVal 29
Db 124 CTGGCTCTCGTGGTGGCGCGTGTCTGTATCTCTCAGCTTGGGGGGCTGCTGGAGGTG 183

Qy 30 ProSerGluThrGluAlaValGlnGlyAsnProMetLysLeuArgCysIleSerCysMet 49
Db 184 GATTCTGAGACCGAGGCGATGTATGGGATGACCTTCAAAATCTCTGTGTATCTCTGTAA 243

Qy 50 LysArgGluGluValGluAlaThrThrValValGluTyrPheTyrArgProGluGlyGly 69
Db 244 CGTGTATGTAGACACCGCGCGAGACCTTACGGAGTGGACCTTCCGCCAGAGGGCACA 303

Qy 70 LysAspPheLeu---IleTyrGluTyrArgAsnGlyHisGlnGluValGluSerPro--- 87
Db 304 GAGGAATTTGTCAAGATCTTACGCTATGAGATGAGGTGCTCGACGTGGAGGAAGATGAG 363

Qy 88 ---PheGlnGlyArgLeuGlnTrpAsnGlySer-----LysAspLeuGlnAspVal 103
Db 364 CGCTTTGAGGCGCGTGTGTGGAAACGCTAGTTCGGGGCACSAAGGACCTGCAGGACCTG 423

Qy 104 SerIleThrValLeuAsnValThrLeuAsnAspSerGlyLeuTyrThrCysAsnValSer 123
Db 424 TCCATCTTCATCACCACCATGTCCCTTACCAACCACTCTGGCGACTACGAATGTCACGTCTAC 483

Qy 124 ArgGluPheGluPheGluAlaHisArgProPheValLysThrArgLeuIleProLeu 143
Db 484 CGTCTCTCTTCTTTGATAATTACGAGCACACACCGCTCGTCAAGAAGATCCACCTG 543

Qy 144 ArgValThrGluGluAlaGlyGluAspPheThrSerValSerValSerGluIleMetMetTyr 163
Db 544 GAGGTGGTGGACAGGCCAACAGATATGGCATCCATCGTGTACAGAGATCATGTATGATAC 603

Qy 164 IleLeuLeuValPheLeuThrLeuTrpLeuLeuIleGluMetIleTyrCysTyrArgLys 183
Db 604 GTGCTCATTTGGTGTAAACCATATGGCTCTGGTGGCGGAGATGCTGTACTCTCAAGAAG 663

Qy 184 ValSerLysAla---GluGluAlaAlaGlnGluAsnAlaSerAspTyrLeuAlaIlePro 202
Db 664 ATTGCTGTGCCACCGAGCTGTGCACAAGAGAAATGCTCGGAATACCTGGCCATTACT 723

Qy 203 SerGluAsnLysGluAsn---SerAlaValProValGluGlu 215
Db 724 TCCGAGAGCAAGAGAACTGTACAGGCGTCCAGGCTGGCTGAA 765

RESULT 5
US-10-533-355-7
; Sequence 7, Application US/10533355
; Publication No. US20050272040A1
; GENERAL INFORMATION:
; APPLICANT: University of Medicine and Dentistry of New Jersey
; APPLICANT: Black, Ira B.
; TITLE OF INVENTION: A METHOD FOR INCREASING SYNAPTIC GROWTH OR PLASTICITY
; FILE REFERENCE: UMD-0016
; CURRENT APPLICATION NUMBER: US/10/533,355

```

; CURRENT FILING DATE: 2005-04-29
 ; PRIOR APPLICATION NUMBER: US 60/422,986
 ; PRIOR FILING DATE: 2002-11-01
 ; NUMBER OF SEQ ID NOS: 16
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 7
 ; LENGTH: 1490
 ; TYPE: DNA
 ; ORGANISM: Rattus norvegicus
 US-10-533-355-7

Alignment Scores:
 Pred. No.: 6,26e-52 Length: 1490
 Score: 472.00 Matches: 105
 Percent Similarity: 64.49% Conservative: 33
 Best Local Similarity: 49.07% Mismatches: 68
 Query Match: 41.99% Indels: 8
 DB: Gaps: 5

US-09-977-579A-2 (1-215) x US-10-533-355-7 (1-1490)

Qy	10	LeuAlaSerLeuValLeuIleTyrTrpValSerValCysPheProValCysValGluVal	29
Db	232	CTGGCTCTCGTGGTGGCGCGTCTGTATCTCTCAGCTGGGGGGCTGGTGGAGGTG	291
Qy	30	ProSerGluThrGluAlaValGlnGlyAsnProMetLysLeuArgCysIleSerCysMet	49
Db	292	GATTCTGAGACCGGAGGAGTGTATGGATGATGACCTTCAAAATCTCTGTATCTCTGTAAG	351
Qy	50	LysArgGluGluValGluAlaThrValValGluTrpPheTyrArgProGluGlyGly	69
Db	352	CGTGTAGTGAGACCGCGGAGACCTTCACGAGTGGACCTTCGCCAGAGGGGACACA	411
Qy	70	LysAspPheLeu---IleTyrGluTyrArgAsnGlyHisGlnGluValGluSerPro---	87
Db	412	GAGGAATTGTCAAGATCTTACGCTATGAGATGAGTGTGCTGAGTGGAGGAAGATGAG	471
Qy	88	---PheGlnGlyArgLeuGlnTrpAsnGlySer-----LysAspLeuGlnAspVal	103
Db	472	CGCTTTGAGGCGCGTGTGTGGACCGTAGTCTGGGCGACCAAGGACCTGCAGGACCTG	531
Qy	104	SerIleThrValLeuAsnValThrLeuAsnAspSerGlyLeuTyrThrCysAsnValSer	123
Db	532	TCCATCTTCATCACCATTGTCACCTACACACTCTGGCGACTACGAATGTCAGTCTAC	591
Qy	124	ArgGluPheGluPheGluAlaHisArgProPheValLysThrThrArgLeuIleProLeu	143
Db	592	CGTCTCTCTCTTTGATTAATTACGACACACACGCGTGTGCAAGAGATCCACCTG	651
Qy	144	ArgValThrGluGluAlaGlyLysAspPheThrSerValValSerGluIleMetMetTyr	163
Db	652	GAGTGTGGACAAAGGCAACAGAGATATGCGATCCATCCGTGTGTCAGAGATCATGATGAC	711
Qy	164	IleLeuLeuValPheLeuThrLeuTrpLeuIleGluMetIleTyrCysTyrArgLys	183
Db	712	GTGCTCATTTGGTGTAAACCATATGCTGTGGCGAGATGGTGTACTGCTACAGAAG	771
Qy	184	ValSerLysAla---GluGluAlaAlaGlnGluAsnAlaSerAspTyrLeuAlaIlePro	202
Db	772	ATTGCTGTGCCCGGAAGCTGTGCACAGAGAATGCTCGGAATACCTGGCCATTACT	831
Qy	203	SerGluAsnLysGluAsn---SerAlaValProValGluGlu	215
Db	832	TCCGAGACCAAGAGACTGTACAGGCGTCCAGGTGCTGAA	873

RESULT 6

US-11-136-527-2402
 ; Sequence 2402, Application US/11136527
 ; Publication No. US20050287570A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wyeth
 ; APPLICANT: Mounts, William M
 ; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes

; FILE REFERENCE: 031896-041000 (AM101086)
 ; CURRENT APPLICATION NUMBER: US/11/136,527
 ; PRIOR FILING DATE: 2005-05-25
 ; PRIOR APPLICATION NUMBER: US 60/574,294
 ; PRIOR FILING DATE: 2005-05-26
 ; NUMBER OF SEQ ID NOS: 362830
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 2402
 ; LENGTH: 1508
 ; TYPE: DNA
 ; ORGANISM: Rattus norvegicus
 US-11-136-527-2402

Alignment Scores:
 Pred. No.: 6,38e-52 Length: 1508
 Score: 472.00 Matches: 105
 Percent Similarity: 64.49% Conservative: 33
 Best Local Similarity: 49.07% Mismatches: 68
 Query Match: 41.99% Indels: 8
 DB: Gaps: 5

US-09-977-579A-2 (1-215) x US-11-136-527-2402 (1-1508)

Qy	10	LeuAlaSerLeuValLeuIleTyrTrpValSerValCysPheProValCysValGluVal	29
Db	232	CTGGCTCTCGTGGTGGCGCGTCTGTATCTCAGCTGGGGGGCTGGTGGAGGTG	291
Qy	30	ProSerGluThrGluAlaValGlnGlyAsnProMetLysLeuArgCysIleSerCysMet	49
Db	292	GATTCTGAGACCGGAGGAGTGTATGGATGATGACCTTCAAAATCTCTGTATCTCTGTAAG	351
Qy	50	LysArgGluGluValGluAlaThrValValGluTrpPheTyrArgProGluGlyGly	69
Db	352	CGTGTAGTGAGACCGCGGAGACCTTCACGAGTGGACCTTCGCCAGAGGGGACACA	411
Qy	70	LysAspPheLeu---IleTyrGluTyrArgAsnGlyHisGlnGluValGluSerPro---	87
Db	412	GAGGAATTGTCAAGATCTTACGCTATGAGATGAGTGTGCTGAGTGGAGGAAGATGAG	471
Qy	88	---PheGlnGlyArgLeuGlnTrpAsnGlySer-----LysAspLeuGlnAspVal	103
Db	472	CGCTTTGAGGCGCGTGTGTGGACCGTAGTCTGGGCGACCAAGGACCTGCAGGACCTG	531
Qy	104	SerIleThrValLeuAsnValThrLeuAsnAspSerGlyLeuTyrThrCysAsnValSer	123
Db	532	TCCATCTTCATCACCATTGTCACCTACACACTCTGGCGACTACGAATGTCAGTCTAC	591
Qy	124	ArgGluPheGluPheGluAlaHisArgProPheValLysThrThrArgLeuIleProLeu	143
Db	592	CGTCTCTCTCTTTGATTAATTACGACACACACGCGTGTGCAAGAGATCCACCTG	651
Qy	144	ArgValThrGluGluAlaGlyLysAspPheThrSerValValSerGluIleMetMetTyr	163
Db	652	GAGTGTGGACAAAGGCAACAGAGATATGCGATCCATCCGTGTGTCAGAGATCATGATGAC	711
Qy	164	IleLeuLeuValPheLeuThrLeuTrpLeuIleGluMetIleTyrCysTyrArgLys	183
Db	712	GTGCTCATTTGGTGTAAACCATATGCTGTGGCGAGATGGTGTACTGCTACAGAAG	771
Qy	184	ValSerLysAla---GluGluAlaAlaGlnGluAsnAlaSerAspTyrLeuAlaIlePro	202
Db	772	ATTGCTGTGCCCGGAAGCTGTGCACAGAGAATGCTCGGAATACCTGGCCATTACT	831
Qy	203	SerGluAsnLysGluAsn---SerAlaValProValGluGlu	215
Db	832	TCCGAGACCAAGAGACTGTACAGGCGTCCAGGTGCTGAA	873

RESULT 7

US-10-750-185-44336
 ; Sequence 44336, Application US/10750185
 ; Publication No. US20050260603A1
 ; GENERAL INFORMATION:
 ; APPLICANT: MMI GENOMICS, INC.


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Qy      143 ----- 143
Db      59104 TCACACGAAGCTCAGCAGACACTCAGGCTGTCTATGCGAGCTGGGTACCCCTTAACC 59163
Qy      144 -ArgValThrGluGluAlaGlyGluAspPheThrSerValValSerGluIleMetMetTy 163
Db      59164 CTGCTGGCCCTCGACGCCAACAGAGACATGGCATCTCGTGTCTGAGATCATGATGTA 59223
Qy      163 rIleLeuLeuValPheLeuThrLeuTrpLeuLeuIleGluMetIleTyrCysTyrArgLy 183
Db      59224 TGTCTCATTTGTGTGTGTGACCATATGGCTCGTGGCAGAGATGATTTACTGCTACAAGAA 59283
Qy      183 sValSerLysAla---GluGluAlaAlaGlnGluAsnAla 195
Db      59284 GATCGCTGCCGCCACCGAGAGACTGTGCACAGGAGATGCG 59323

RESULT 10
US-11-112-908-55
; Sequence 55, Application US/11112908
; Publication No. US20050260659A1
; GENERAL INFORMATION:
; APPLICANT: Harris, Lisa M.
; TITLE OF INVENTION: Breast Cancer Biomarkers
; FILE REFERENCE: 04-164-US
; CURRENT APPLICATION NUMBER: US/11/112,908
; CURRENT FILING DATE: 2005-04-22
; PRIOR FILING DATE: 2005-04-22
; PRIOR FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: US 60/564,758
; PRIOR FILING DATE: 2004-06-01
; PRIOR APPLICATION NUMBER: US 60/575,978
; PRIOR FILING DATE: 2004-11-30
; PRIOR APPLICATION NUMBER: US 60/631,702
; PRIOR FILING DATE: 2004-12-07
; PRIOR APPLICATION NUMBER: US 60/633,826
; NUMBER OF SEQ ID NOS: 511
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 55
; LENGTH: 193789
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-112-908-55
Alignment Scores:
Pred. No.: 6,96e-08 Length: 193789
Score: 165.50 Matches: 56
Percent Similarity: 47.13% Conservative: 26
Best Local Similarity: 32.18% Mismatches: 45
Query Match: 14.72% Indels: 48
DB: 7 Gaps: 7

US-09-977-579A-2 (1-215) x US-11-112-908-55 (1-193789)
Qy      67 GluGlyGlyLysAspPheLeuIleTyrGlu-TyrArgAsnGlyHisGlnGluValGluSe 86
Db      108996 GAAGGAGGTATTCATTTTACAAATTGAAGAAACAGAGG-----CCTAGACACATTGATC 109049
Qy      86 rProPheGlnGlyArgLeu-----GlnTrp-----AsnGlySerLysAs 99
Db      109050 ACTTGGCGAAGGTACACACAGCTGGCCAGTGGCAGAGCCGCTTGTGAACCTGAGCCTTCT 109109
Qy      99 pLeuGlnAspValSerIle-----ThrValLeuAsnValThrLeuAsnAspSerGlyLe 117
Db      109110 GGTTGCAGAGCTACCGGCTTTTAGGCACCGTGTCTGAGGCGCTCCAG-AATGACACAGATGT 109168
Qy      117 uTyrThrCysAsnValSerArgGluPheGluAlaHisArg----- 132
Db      109169 GGCCTCGAGTTACACAGGAGGCGAGGTGAGGCGGACCCCAACACAGAGCCTACCAAGGCT 109228
Qy      133 -----ProPheValLysThrThrArgIleProLeu----- 143
Db      109229 GGGTATTAAATAACACAGTGCATACACAGGCCCGGAGGGTTGAGGCCACTCATCCAAGC 109288

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Qy      143 ----- 143
Db      109289 TCACACGAAGCTCAGCAGACACTCAGGCTGTCTATGCGAGCTGGGTACCCCTTAACC 109348
Qy      144 -ArgValThrGluGluAlaGlyGluAspPheThrSerValValSerGluIleMetMetTy 163
Db      109349 CTGCTGGCCCTCGACGCCAACAGAGACATGGCATCTCGTGTCTGAGATCATGATGTA 109408
Qy      163 rIleLeuLeuValPheLeuThrLeuTrpLeuLeuIleGluMetIleTyrCysTyrArgLy 183
Db      109409 TGTCTCATTTGTGTGTGTGACCATATGGCTCGTGGCAGAGATGATTTACTGCTACAAGAA 109468
Qy      183 sValSerLysAla---GluGluAlaAlaGlnGluAsnAla 195
Db      109469 GATCGCTGCCGCCACCGAGAGACTGTGCACAGGAGATGCG 109508

RESULT 11
US-11-080-991-111
; Sequence 111, Application US/11080991
; Publication No. US20050266437A1
; GENERAL INFORMATION:
; APPLICANT: Veiby, Petter Ole
; TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF BREAST
; TITLE OF INVENTION: AND OVARIAN CANCER
; FILE REFERENCE: MRI-039
; CURRENT APPLICATION NUMBER: US/11/080,991
; CURRENT FILING DATE: 2005-03-11
; PRIOR FILING DATE: 2005-03-11
; PRIOR FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: US/10/176,847
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 111
; LENGTH: 673
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-080-991-111
Alignment Scores:
Pred. No.: 3,28e-09 Length: 673
Score: 147.00 Matches: 57
Percent Similarity: 41.44% Conservative: 35
Best Local Similarity: 25.68% Mismatches: 80
Query Match: 13.08% Indels: 50
DB: 7 Gaps: 9

US-09-977-579A-2 (1-215) x US-11-080-991-111 (1-673)
Qy      7 LeuPheProLeuAlaSerLeuValLeuIleTyrTrpValSerValCysPheProValCys 26
Db      89 CTTTGGCCTATAGCAGCT---GTGGAAATTTATACCTCCCGGTG----- 130
Qy      27 ValGluValProSerGluThrGluAlaValGlnGlyAsnProMetLysLeuArgCysIle 46
Db      131 -----CTGGAGGCTGTTAATGGGACAGATGCTCGTTAAATGACT 172
Qy      47 SerCysMetLysArgGluGluValGluAlaThrValValGluTrpPheTyrArgPro 66
Db      173 TTCTCCAGCTTTGCCCTGTGGGTGATGCTCTAAACAGTGACC---TGGAAATTTTCGTCT 229
Qy      67 ---GluGlyGly---LysAspPheLeuIleTyrGluTyrArgAsnGlyHisGlnGluVal 84
Db      230 CTAGACGGGGGAGCCTGAGCAGTTGTTATCTTACCACATAGATCCCTTCCAAACCCATG 289
Qy      85 GluSerProPheGlnGlyArgLeuGlnTrpAsnGlySerLysAspLeuGlnAspValSer 104
Db      290 AGTGGGGCGTTTAAAGNCCGGGTCTTGGGATGGGAAATCCTGAGCGGTACGATGCCCTCC 349
Qy      105 IleThrValLeuAsnValThrLeuAsnAspSerGlyLeuTyrThrCysAsnValSerArg 124
Db      350 ATCCTTCTCTGGAAACATGCGAGTTTCACGACCAATGGGACATACACCTCCAGGTGAAGAAC 409

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Qy 125 GluPheGluPheGluAlaHisArgProPheValIysThrThrArgLeuIleProLeuArg 144
Db 410 -----CCACCTGAT 418
Qy 145 ValThrGluGluAlaGlyGluAspPheThrSerValVal-----SerGlu 159
Db 419 GTTGATGGGTGATAGGGGAGATCCGGCTCAGCGTCGTGCACACTGTACGCTTCTCTGAG 478
Qy 160 IleMetMetTyrIleLeuLeuVal-----PheLeuThrLeuTrpLeu 173
Db 479 ATCCACTTCTCGCTCTGCGCATTTGGCTCTCGCTGTGCACACTGATGATCATATAAGTAAT 538
Qy 174 LeuIleGluMetIleTyrCysTyrArgLysValSerLysAlaGluGluAlaGlnGlu 193
Db 539 GTAGTGGTCTCTTCCACANTTACCGGAAAGCGATGGCGCGAAGAGCT----- 589
Qy 194 AsnAlaSerAspTyrLeuAlaIleProSerGluAsnLysGluAsnSerAlaValProVal 213
Db 590 -----CATAAAGTGTGGAGATAAAATCAAAAGAGAGAGAAAGGCTCAACCAA 637
Qy 214 GluGlu 215
Db 638 GAGAAA 643

RESULT 12

US-10-131-826A-487
; Sequence 487, Application US/10131826A
; Publication No. US20050245730A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330RIC128
; CURRENT APPLICATION NUMBER: US/10/131,826A
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550

; SEQ ID NO 487
; LENGTH: 1371
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-131-826A-487
Alignment Scores:
Pred. No.: 9.8e-09 Length: 1371
Score: 147.00 Matches: 57
Percent Similarity: 41.44% Conservative: 35
Best Local Similarity: 25.68% Mismatches: 80
Query Match: 13.08% Indels: 50
Gaps: 9
US-09-977-579A-2 (1-215) x US-10-131-826A-487 (1-1371)
Qy 7 LeuPheProLeuAlaSerLeuValLeuIleTyrTrpValSerValCysPheProValCys 26
Db 181 CTTTGGCTATAGCAGCT---GTGGAAATTATACCTCCCGGGTG----- 222
Qy 27 ValGluValProSerGluThrGluAlaValGlnGlyAsnProMetLysLeuArgCysIle 46
Db 223 -----CTGGAGCGCTGTTAATGGGACAGATGCTCGGTTAAATGCAC 264
Qy 47 SerCysMetLysArgGluGluValGluAlaThrThrValValGluTrpPheTyrArgPro 66
Db 265 TTCTCCAGCTTTGCCCTGTGGGTGATGCTCTAACAGTGACC---TGGAAATTTGCTCCT 321
Qy 67 ---GluGlyGly---LysAspPheLeuIleTyrGluTyrArgAsnGlyHisGlnGluVal 84
Db 322 CTAGACGGGGACCTGAGCAGTTTGTATTCTACTACCATAGATCCCTTCCAACCCCATG 381
Qy 85 GluSerProPheGlnGlyArgLeuLysTrpAsnGlySerLysAspLeuGluAspValSer 104
Db 382 AGTGGGGGTTTAAAGGACCGGGTGTCTTGGGATGGGAATCTCTGAGCGGTACGATGCCCTCC 441
Qy 105 IleThrValLeuAsnValThrLeuAsnAspSerGlyLeuTyrThrCysAsnValSerArg 124
Db 442 ATCCTTCTCTCGAAACTGCAGTTTCGACGACAATGGGACATACACCTGCAGGTGAAGAAC 501
Qy 125 GluPheGluPheGluAlaHisArgProPheValLysThrThrArgLeuIleProLeuArg 144
Db 502 -----CCACCTGAT 510
Qy 145 ValThrGluGluAlaGlyGluAspPheThrSerValVal-----SerGlu 159
Db 511 GTTGATGGGTGATAGGGGAGATCCGGCTCAGCGTCGTGCACACTGTACGCTTCTCTGAG 570
Qy 160 IleMetMetTyrIleLeuLeuVal-----PheLeuThrLeuTrpLeu 173
Db 571 ATCCACTTCTCGGCTCTGCCCATTTGGCTCTGCTGTGCACCTGATCATATAAGTAAT 630
Qy 174 LeuIleGluMetIleTyrCysTyrArgLysValSerLysAlaGluGluAlaGlnGlu 193
Db 631 GTAGTGGTCTCTTCCACANTTACCGGAAAGCGATGGCGCGAAGAGCT----- 681
Qy 194 AsnAlaSerAspTyrLeuAlaIleProSerGluAsnLysGluAsnSerAlaValProVal 213
Db 682 -----CATAAAGTGTGGAGATAAAATCAAAAGAGAGAGAAAGGCTCAACCAA 729
Qy 214 GluGlu 215
Db 730 GAGAAA 735
RESULT 13
US-10-131-826A-529
; Sequence 529, Application US/10131826A
; Publication No. US20050245730A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc


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Qy 82 GlnGluValGluSerProPheGlnGlyArgLeuGlnTrpAsnGlySerLysAspLeuGln 101
Db 434 CTGAAGCTGGAGCGG---TTTGGAGACCGCGTAGAGTTCTCGGGGAACCCAGTAAGTAC 490
Qy 102 AspValSerIleThrValLeuAsnValThrLeuAsnAspSerGlyLeuTyrThrCysAsn 121
Db 491 GACGTGTCAAGTACTCTTAAGAACGTGACGTAGACGAGGAGGCAATTACAACCTGTAC 550
Qy 122 ValSerArgGluPheGluPheGluAlaHisArgProPheValLysThrThrArgLeuIle 141
Db 551 ATCACCAAC-----CCTCCAGACCGCCACCGTGGCCATGGCAAGATCTACCTGCAGTGC 604
Qy 142 ProLeuArgValThrGluGluAlaGlyGluAspPheThrSerValValSerGluIleMet 161
Db 605 CTTCTWGAAGTGCCTCCACCGGACGGRACCKCCACGGTGGCAGTCATCGTGGGCTCAGTG 664
Qy 162 MetTyrIleLeuLeuValPheLeuThrLeuTrpLeuLeuIleGluMetIleTyrCysTyr 181
Db 665 GGGGTTTCTGTCGTGTGTCTATM-----TTTGTGTGTGTGTGTGTCAATGTGTG 715
Qy 182 ArgLysValSerLysAlaGluGluAlaAlaGlnGluAsnAlaSerAspTyrLeuAlaIle 201
Db 716 AGGAGG-----AAAAAGACGACAGAGCTGAGCAGCATGACVCTGAAGACC 760
Qy 202 ProSerGluAsnLysGluAsnSerAlaValProValGluGlu 215
Db 761 GAAGAGGAAGGCAAGACGGATGGCGGAGGGCAACCGCGGAAGAT 802

RESULT 15
US-10-374-954-6
; Sequence 6, Application US/10374954
; Publication No. US20050260576A1
; GENERAL INFORMATION:
; APPLICANT: Vanderbilt University
; APPLICANT: George, Alfred L
; APPLICANT: Lossin, Christoph
; TITLE OF INVENTION: HETEROLOGOUS EXPRESSION SYSTEM FOR STUDYING RECOMBINANT HUMAN
; TITLE OF INVENTION: BRAIN VOLTAGE-GATED SODIUM CHANNEL, SCN1A
; FILE REFERENCE: 1242/41/2
; CURRENT APPLICATION NUMBER: US/10/374,954
; CURRENT FILING DATE: 2003-02-25
; PRIOR APPLICATION NUMBER: US 60/359,382
; PRIOR FILING DATE: 2002-02-25
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 648
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(648)
US-10-374-954-6
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Alignment Scores:
Pred. No.: 0.000222 Length: 648
Score: 110.50 Matches: 55
Percent Similarity: 45.33% Conservative: 42
Best Local Similarity: 25.70% Mismatches: 88
Query Match: 9.83% Indels: 29
DB: Gaps: 11

US-09-977-579A-2 (1-215) x US-10-374-954-6 (1-648)

Qy 2 ProAlaPheAsnArgLeuPheProLeuAlaSerLeuValLeuIleTyrTrpValSerVal 21
Db 28 CTGCGCTTCAGC-----CTCAGCGGGCTCATGCTCTTTTTC-----TCTTIG 69
Qy 22 CysPhePro-----ValCysValGluValProSerGluThrGluAlaValGlnGly 38
Db 70 GTGCCACACGAGCGGAGCATGGAGTTCACAGTACTTCCACACCTCAACCTCAATGGC 129

39 AsnProMetLysLeuArgCysIle-----SerCysMetLysArgGluGluValGluAla 56
130 TCTGACGCCCGCTGCCCTGCACCTTCAACTCTCTGTACACAGTGAACACCAACAGTTTC 189
57 ThrThrValValGluThrPheTyrArgProGluGlyGly-----LysAspPheLeu 73
190 TCC-----CTGAACCTGGACTTACCAGGAGTGCACCAACTGCTCTGAGGAGATGTTCTC 243
74 IleTyrGluTyrArgAsnGlyHisGlnGluValGluSerProPheGlnGlyArgLeuGln 93
244 CAGTTCGCGATGAAGATCATTAACCTGAAGCTGGAGCGG---TTTCAAGACCGCGTGGAG 300
94 TrpAsnGlySerLysAspLeuGlnAspValSerIleThrValLeuAsnValThrLeuAsn 113
301 TTCTCAGGGAACCCAGCAAGTACGATGTGTGGTGATGCTGAGAAACGTCAGCCGGAG 360
114 AspSerGlyLeuTyrThrCysAsnValSerArgGluPheGluAlaHisArgPro 133
361 GATGAGGGGATTTACAACCTGCTACATCATGAAC-----CCCCCTGACCGCCACCGTGGC 414
134 PheValLysThrThrArgLeuIleProLeuArgValThrGluGluAlaGlyGluAspPhe 153
415 CATGGCAG-----ATCATCTGCAGGTCTCATGGAAGAGAGCCCTGAGCGG 462
154 ThrSerValValSerGluIleMetMetTyrIleLeuLeuValPheLeuThrLeuTrpLeu 173
463 GACTTCCACGGTGGCGGTGATTGTGGTGCTCCGTCGGGGGGCTTCTCGCTGTGTGTCATC 522
174 LeuIleGluMetIleTyr---CysTyrArgLysValSerLysAlaGluGluAlaGln 192
523 TTGCTGTGTGTGTGTGTCAAGTGTGTGAGGAGA-----AAAAAGAGCAG 567
193 GluAsnAlaSerAspTyrLeuAlaIleProSerGluAsnLys 206
568 AAGCTGAGCACACATGATGACCTGACACCGAGGAGGAGGGCAG 609

Search completed: January 5, 2006, 17:54:07
Job time : 269 secs
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